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RESULT OF RESULT
RESULT 7
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Q8UE
AC Q8UE
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DT 01-J
DT 01-J
DT 01-J
DT 25-C
DE HYPOC
GN OTGE
OC Rh1
CN NCB1
CN
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QBUED4; Q7CYF9;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002; (TrEMBLrel. 28, Last annotation update)
25-OCT-2004; (TrEMBLrel. 28, Last annotation update)
Hypothetical protein Atul226 (AGR C 3351p).
OrderedLoccusNames=AGR C 3351p, Atul226;
Agrobacterium tumefacTens (strain C58 / ATCC 33970).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Rhizobiaceae, Anizobium/Agrobacterium group; Agrobacterium.
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EMBL, ALS91988; CAC46316.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
InterPro, IPR000379; Ser estrs.
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Q92PK7;
01-DEC-2001
                                                                                                                                                                 MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., W. Z., Romero P., Gordon D. Raymond C., Kouse G., Saenphimmachak C., W. Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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Hypothetical protein SMc00528.
ORFNames=SMc00528;
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                           "The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                                                                                         Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=176299;
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STRAIN-1021;
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01-OCT-2003
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    294:2317-2323(2001).
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(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 25, Last annotation
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85.7%;
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Pred. No.
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24;
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RESULT 9
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SEQUENCE
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PubMed=15210978; DOI=10.1073/pnas.0305659101;

Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ardell Alsmark U.C.M., Frank A.C., Naeslund A.K., Handley S.A., Huvet M. Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huvet M. La Scola B., Holmberg M., Andersson S.G.E.;

"The louse-borne human pathogen Bartonella quintana is a genomic derivative of the zoonotic astronella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

EMBL; BX897700; CAF26085.1; -.

EQ.; GO:000324; F:cattalytic activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q6FZW3;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-21608551; PubMed=11743194; DOI=10.1126/science.1066803; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L. Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
OrderedLocusNames=BQ05930;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Bartonella quintana (Rochalimaea quintana).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
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SEQUENCE FROM N.A.
STRAIN=Cereon;
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                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=803;
                                                                                                                                                                                                                                                                                                                                                                                                                          Bartonellaceae; Bartonella.
                                                                                                                                                                                                                        InterPro; IPR000379; Ser_estrs.
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; B97580; B97580.
G0:0003824; F:catalytic activity; IEA.
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226 AA;
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cal protein; Complete proteome.
225 AA; 25084 MW; 1B7BDF5600841833 CRC64;
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                                                                                                                                                                                               25373 MW;
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85.7%;
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Pred. No. 24;
1; Mismatches
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Pred. No. 24;
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C., Mullin L.,
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Q6G3B7 Q6G3B7;

PRELIMINARY;

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PubMed=15210978; DOI=10.1073/pnas.0305659101;

A Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Arc Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley S.A., Huv La Scola B., Holmberg M., Andersson S.G.E.;

"The louse-borne human pathogen Bartonella quintana is a genc derivative of the zoonotic agent Bartonella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

R EMBL; BX897699; CAF27664.1; -.

R GO; GO:0003824; F:catalytic activity; IEA.

R InterPro; JPR000379; Ser estrs.

Complete proteome; Hypothetical protein.

SEQUENCE 226 AA; 25230 MW; 7216738444690A60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q98NR9;
01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2001 (TrEMBLrel. 18,
01-OCT-2003 (TrEMBLrel. 25,
M110014 protein.
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
Hypothetical protein.
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Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                            Complete
                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                       DNA Res.
                                                                                                                                                                                                                                                                                                                        "Complete genome structure Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasan Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
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                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                     GO:0003824; F:catalytic activity;
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                                                                                           Similarity 6; Conser
                                                                                                                                                                                      proteome.
228 AA;
                                                                                                                                                                                                                                                                                                       7:331-338(2000).
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                                             XHPOFGG 8
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  PHPOFGG
                                                                                                                                                                                                                          IPR000379; Ser_estrs
                                                                                             Conservative
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                                                                                                                                                                                      25544 MW;
                                                                                                              88.6%;
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Pred. No. 24;
1; Mismatches
                                                                                           Score 39; DB
Pred. No. 24;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                     the
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                                                                                             Indels
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STANDARD; PRT; 379 AA.

D PSII_SCHPO STANDARD; PRT; 379 AA.

Q 09972; 09UU92;

TO 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 44, Last sequence update)

DT 05-UUI-2001 (Rel. 44, Last annotation update)

DT 05-UUI-2004 (Rel. 44, Last annotation update)

DT 05-UUI-2004 (Rel. 44, Last annotation update)

DT 05-UUI-2004 (Rel. 47, Last annotation update)

DT 05-UUI-2004 (Rel. 48, Last annotation update)

DT 05-UUI-2004 (Rel. 49, Last anno
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PSI1_SCHPO
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Best Local
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STRAIN=FI-985;
Bagga S., St Leger I
Submitted (OCT-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q96UF7;
01-DEC-2001
01-DEC-2001
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GO; GO:0004289; F:subtilase activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR000209; Pept_S8 S53.
InterPro; IPR0090209; Prot inh propept.
InterPro; IPR009020; Prot inh S8A.
Pfam; PP00082; Peptidase S8; I.
Pfam; PP09922; Subtilisin N; 1.
Prant Trot of the S8A.
Pfam; PP09922; Subtilisin N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; Clavicipitaceae; mitosporic Clavicipitaceae; Metarhizium.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-MAR-2004 (TrEMBLrel. 26, Last annotation
Subtilisin-like serine protease PRIB (Fragme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q96UF7
                                                                                                                                                                                                                                                                                                                        MEDLINE=95290501; PubMed=77726(Park S.-K., Chon S.-K., Yoo H. "A cDNA of Schizosaccharomyces
MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724; Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewari Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
                                                                                                                                                                                                                                                                                              protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896;
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(OCT-2001) to
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330 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                             PubMed=7772606; DOI=10.1016/0167-4781(95)00063-M; S.-K., Yoo H.-S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330
34673 MW; 09E294C2864E9130 CRC64;
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RESULT 13
Q96UF9
ID Q96UF
AC Q96UF
DT 01-DE
DT 01-DE
DT 01-DE
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Best Local S
Matches 6
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GeneDB_Spenche; SPCC830.07c; -.

InterPro; IPR002939; DnaJ_C.

InterPro; IPR001623; DnaJ_N.

InterPro; IPR008971; HSP40_DnaJ_pep.

InterPro; IPR00395; Hsp_DnaJ_pep.

Pfam; PF00226; DnaJ_C; 1.

Pfam; PF00456; DnaJ_C; 1.

PRINTS; PR00625; DNAJ_SPROTEIN.

SMART; SM00271; DnaJ; 1.
Q96UF9;
Q96UF9;
01-DEC-2001
01-DEC-2001
01-MAR-2004
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or send an
                                                                                                                                        CONFLICT
SEQUENCE
                                                                                                                                                                       PROSITE; PS00636; DNAJ 1; 1.
PROSITE; PS50076; DNAJ 2; 1.
Cell cycle; Chaperone; DNA-binding.
                                                                                                                                                                                                                                                                                  EMBL; L3775j, AAA74732.1; -.
EMBL; AL109850; CAB52880.1; -.
PIR; S55900, S55900.
PIR; T41633; T41633.
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                                                                                        μ
                                                                                                       Similarity 6; Conserv
                                                                         RSHPSFGG 194
                                                                                       RXHPQFGG 8
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; 91
379 AA;
(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                        Conservative
                                PRELIMINARY;
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                                                                                                                                        91 G
40260 MW;
                                                                                                                88.6%;
75.0%;
19,
Created)
Last sequence update)
Last annotation updat
                                                                                                                Score 39;
Pred. No.
                                                                                                                                       J-domain.
Gly-rich.
G -> C (in Ref. 1).
G => C (50 Ref. 1).
                                                                                                        Mismatches
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                                                                                                                        DB 1; Length 379;
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update)
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RESULT 14
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Best Local S
Matches 6
                                    STRAIN-ARSE 2575;

Bagga S., Screen S.E., St Leger R.J.;

Leger R.J.;

EMBL; AUZ89823; CAB95012.1;

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0004289; F:puroteolysis and peptidolysis; IEA.

GO; GO:0006508; P:puroteolysis and peptidolysis; IEA.

GO; GO:0006500065009; P:puroteoly
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HSSP; P06873; I1C6.

GO; GO:0008233; F:peptidase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:0004289; F:subtilase activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IE;

InterPro; IPR000183; Decarbxy1se2.

InterPro; IPR000209; Pept S8 $53.

InterPro; IPR00920; Prot_inh_propept.

InterPro; IPR010259; Prot_inh_SA.

Pfam; PF00082; Subtiliasin N; 1.

PRINTS; PR0723; Subtiliasin N; 1.

PRINTS; PR0723; SUBTILISIN.
Protease.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9P3Y1 PRELIMINARY; PRT; 385 AA.
Q9P3Y1;
Q1-OCT-2000 (TYEMBLYEL. 15, Created)
Q1-OCT-2000 (TYEMBLYEL. 15, Last sequence update)
Q1-MAR-2004 (TYEMBLYEL. 26, Last annotation updat subtilisin-like protease PRIB.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metarhizium anisopliae var. anisopliae.
Bukaryota; Rungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae;
mitosporic Clavicipitaceae; Metarhizium.
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Submitted (OCT-2001) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=92636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=prlB;
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PROSITE; PS00136; SUBTILASE_ASP; 1.
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Metarhizium anisopliae var. anisopliae.
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385 AA;
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Best Local S
Matches 6
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C STRAIN-ARSEF 2575;
A JOSHI L.S.t., Leger R.J., Roberts D.W.;
B SUBMITTED 196873; P.S. Leger R.J., I.E.

R EMBL; U59484; AAC49831.1; -.

R GO; GO:0006333; F:peptidase activity; IEA.
R GO; GO:0004289; F:subbilase activity; IEA.
R GO; GO:0004289; F:subbilase activity; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR000183; Decarbxylse2.
R InterPro; IPR000183; Decarbxylse2.
R InterPro; IPR000209; Pept_S8 S53.
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Best Local Similarity
Matches 6; Conserv
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NON TER
SEQUENCE
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STRAINARSEF 2575;

MEDLINE=97473490; PubMed=9332344; DOI=10.1016/S0378-1119(97)00132-7;

MEDLINE=97473490; PubMed=9332344; DOI=10.1016/S0378-1119(97)00132-7;

JOSHI L., St Leger R.J., Roberts D.W.;

"Isolation of a cDNA encoding a novel subtilisin-like protease (Pr1B) from the entomopathogenic fungus, Metarhizium anisopliae using differential display-RT-PCR.";

Gene 197:1-8(1997).
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Subtilisin-like protease PriB (Fragment).
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Clavicipitaceae;
mitosporic Clavicipitaceae; Metarhizium.
NCBI_TaxID=5530;
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                                                                                                                                                                Local Similarity 85.7
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386 AA; 40031 MW; E805E0751C471568 CRC64;
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                                                                                                                                                        88.6%; Score 39; DB 2; Length 386;
85.7%; Pred. No. 42;
tive 1; Mismatches 0; Indels
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1; Mismatches
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Search completed: March 2, 2005, 12:44:18 Job time: 30.7236 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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A Geneseq_16Dec04:*
1: geneseqp1980s:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	v	4	ω	2	1	No.	1
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invention: ividual mode st one moti- eptavidin b- ification o- ification o- ification o- on protein ongly to sti- onger bindi- not be esse trollable b- from dilute from dilute that of a si	2003-0 isolate ein, colles.	(-2001; (-2001; ) INST		
The invention relates to an is individual modules separated by least one motif His-Pro-X wher streptavidin binding modules, purification of recombinant fue.g. on protein chips or microstrongly to streptavidin, with strongly to streptavidin, with the stronger binding than a single (I) does not interfere with the may not be essential to remove controllable binding properties. Pp from dilute solution in batthan column methods and result is that of a streptavidin tag i	2003-031166/03. solated peptide in, comprises a es. osure; Page 2;	-	dard; (first tag pe prote	
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Best Local S
Matches 6
                                                                                                                                                                                                                                            Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                        This peptide comprises the strep-tag peptide that is recognised by streptavidin. A form of novel growth factor (HIL (see AAW32479) was generated by PCR that contains a FLAG epitope (see AAW32484) at its N-terminus and the strep-tag at its C-terminus. The construct is designated LHL.seq (see AAW32481), where L is the immunoglobulin binding entity from peptostreptococcus magnus and H is residues 42-62 of hen egg lysozyme. The strep-tag was used for purification of LHL.seq over a streptavidin column. Thus, the LHL-seq was not purified on the basis of binding lamunoglobulin, thereby eliminating potential contamination by other bacterial proteins which also bind immunoglobulins. LHL.seq has identical activity to that of LHL, and can be used in novel methods for the generation of catalytic antibodies
                                                                                                                                                                                                                                                                                                                           Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 3; Page 40; 109pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New catalytic antibody precursors -
binding portion which can induce B-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-489572/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AMRA-) AMRAD OPERATIONS PTY LTD
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27-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Catalytic antibody; growth factor; B-cell mitogenesis; LHL; L protein; hen egg lysozyme; strep-tag; purification.
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                                                                                                                                                                                                                   Similarity 6; Conserv
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                                                                                                                                               XHPQFGG 8
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                                                                                                             RHPQFGG 9
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97AU-00005375.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tarlinton DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ecursors - comprising a B-cell surface molecule induce B-cell mitogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                   Score 39; DB Pred. No. 1.8e
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Pred. No. 1.8e+06;
1; Mismatches 0;
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW59211 and AAW59212 are ligands used in a method to assay binding affinity of streptavidin mutants. These method have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Axg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or sensor chips
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9 AA;
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                                                                                          Synthetic.
                                                                                                                                            transgenic animal; scrapie; Creut:
bovine spongiform encephalopathy;
                                                                                                                                                                               Prion; epitope; FIAG; Strep; poly-histidine; haemagglutinin; recombinant; transgenic animal; scrapie; Creutzfeldt-Jakob disease; CJD;
                                                                                                                                                                                                                                                                         Strep peptide epitope used in an epitope tagged prion protein construct.
                                                                                                                                                                                                                                                                                                                                     05-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW44010 standard; peptide; 9
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6; Conserv
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Pred. No. 1.8e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents an artificial Strep peptide epitope. It is used CC in a recombinant nucleic acid construct encoding an epitope-tagged prion protein (Prp). The construct comprises a first nucleic acid sequence CC encoding an amino acid sequence of a biologically active protein fragment and a second nucleic acid sequence encoding a heterologous epitope CC domain. The heterologous epitope domain is a peptide selected from a peptide group of FLAG, Strep, poly-histidine, human c-myc peptide CC recognised by monoclonal antibody 9E10 and haemagglutinin peptide CC recognised by monoclonal antibody 9E10 and haemagglutinin peptide CC recognised by monoclonal antibody 12CAS. The protein has two different three concirmation conformations and the epitope domain is spatially positioned CC dimensional conformations and the epitope domain is more exposed in a CC first confirmation relative to a second conformation. The nucleic acid CC construct may be used for the production of transgenic animals or cells CC that are useful in a method for distinguishing between different CC conformational shapes of a protein. These methods are particularly useful cin studying diseases caused by prion proteins, e.g. Creutzfeldt-Jakob CC disease (CJD), scrapie and bovine spongiform encephalopathy (BSE)
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Best Local
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                                                                                                                                                               Growth factor precursor; B-cell surface; T cell surface; CAb; hepatit: catalytic antibody; immunoglobulin; tumour necrosis factor; influenza rheumatoid arthritis; toxic shock syndrome; viral docking receptor; human immune virus; tumour-specific antigen; amyloid plaque; myeloma; Alzheimer's disease; IGE; allergy; asthma; drug detoxification; autoimmune; inflammatory disease; gene therapy; strep-tag.
 19-SEP-1997;
                                                                01-APR-1999.
                                                                                                  WO9915563-A1
                                                                                                                                                                                                                                                                                  Strep-tag sequence
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                               18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                     AAY06914 standard; peptide; 9 AA.
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97AU-00009306
                               98WO-AU000783.
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Pred. No.
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1.8e+06;
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Best Local
New nucleic acid encoding chimeric proteins with self-assembly properties, useful e.g. for diagnosis and treatment of prion d
                                                                                                                                                                                                                                                                                                                                  SCHAG; self-coalesce; higher-order aggregate; amyloidogenic domain; aggregation; fibril; phenotypic alteration; gene therapy; disease resistance; plant pigmentation; prion disease.
                                                   WPI; 2001-061723/07
                                                                                                                                                           09-JUN-1999;
                                                                                                                                                                                           09-JUN-2000; 2000WO-US015876.
                                                                                                                                                                                                                               14-DEC-2000
                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                      AMino acid sequence of a Strep epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB30795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB30795 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a growth factor precursor that comprises B-cell surface binding part, T cell surface binding part, antigen cleavable by a catalytic antibody (CAb); and a peptide comprising heavy and light chains of immunoglobulin. When the antigen is cleaved the B cell surface part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Growth factor precursor cleaved by antigen-specific catalytic antibody.
                                                                                    Lindquist S,
                                                                                                                                                                                                                                                                WO200075324-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence represents a strep-tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 42; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koentgen F, Suess GM,
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                                                                                Li L,
                                                                                                                                                          99US-0138833P.
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85.7%;
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                                                                                      Liu J,
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Pred. No. 1.8e+06;
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                                                                                      Sondheimer N,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents an epitope, which may be attached to CC chimeric polypeptides of the invention. The specification describes CC chimeric polypeptides which comprise at least one SCHAG (self-coalesces into higher-order aggregates) amino acid sequence fused in frame with a CC polypeptide of interest (which is other than a marker protein, a CC specification also describes chimeric polypeptides that comprises an CC entrologenic domain that causes aggregation into fibrils. The chimeric polypeptides are used to prepare polymers with multiple reactivities, CC e.g. derivatised with enzymes, or specific binding partners, and useful CC engene therapy, protein production, imparting disease resistance to plants, or altering plant pigmentation and for diagnosis and treatment of prion
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Best Local S
Matches 6
The invention describes a method of producing a peptide or its derivative, comprising using a reaction system for transcribing DNA RNA and translating the RNA, or a reaction system for in vitro RNA translation, where a part or all of protein components constituting
                                                                                                                                                                                                           and tran
                                                                                                                                                  Disclosure; Page 44;
                                                                                                                                                                                                                              Producing peptides, and translating RNA,
                                                                                                                                                                                                                                                                                                           WPI; 2002-599608/64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-2000; 2000JP-00401417.
15-JAN-2001; 2001JP-00006910.
27-JUL-2001; 2001JP-00227094.
26-SEP-2001; 2001JP-00294795.
                                                                                                                                                                                                                                                                                                                                                                                                                     (POST-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide production method; in vitro translation; in vitro transcription;
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                                                                                                                                                                                                                                                                                                                                                            Þ
                                                                                                                                                                           ng peptides, using reaction system for transcribing DNA into RNA nslating RNA, or for direct in vitro RNA translation, where components are labeled with a label pair adhering to each other
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                                                                                                                                                                                                                                                                                                                                                            Shimizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHPQFGG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aggregates, fibrils and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method associated strep-tag
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                                                                                                                                                102pp;
                                                                                                                                                                                                                                                                                                                                                            Ueda
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Pred. No.
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1.8e+06;
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Sequence 9 AA,

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Matches 6
         This invention relates to recombinant vectors, comprising a promoter sequence and a nucleotide sequence encoding a first protein, which is a membrane protein, or multisubunit protein. The recombinant vector is to the crystallisation of proteins that are otherwise difficult to crystallise. This sequence represents the Strep-tag nonapeptide. This linker acts as a bridge between subunit IV and the foreign fusion protein of plasmid pMB908 (see AAH99982)
                                                                                                                                       Claim 19;
                                                                                                                                                     New recombinant vectors comprising promoter and nucleotide suseful in methods of crystallization, particularly for the crystallization of proteins that are otherwise difficult to
                                                                                                                                                                                                                                          Iwata S,
                                                                                                                                                                                                                                                                                                                                                     05-MAY-2000; 2000SE-00001666.
02-JUN-2000; 2000US-0209331P.
28-JUN-2000; 2000SE-00002432.
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                                                                                                                                                                                                                                                                                                                                   (IMCO-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crystal lattice; crystallography; three dimensional structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strep-tag nonapeptide linker sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reaction system are labeled with one of a pair of substances adhering to each other and the other substance of the pair is used as an adsorbent for capturing labeled protein components after translation. The produced protein is efficiently isolated at a high purity from the reaction system, and at the same time, the problem of consumption of energy in the reaction system is resolved. This sequence represents a strep-tag which binds to streptayidin and can be used to purify peptides in the peptide
                                                                                                                                                                                                                                                                      SEJL/)
                                                                                                                                                                                                                                                                                                            BYRN/)
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IWATA S.
BYRNE B.
JORMAKKA |
ABRAMSON
                                                                                                                                                                                                                                                                  SEJLITZ T.
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                                                                                                                                   Page 30; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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                                                                                                                                                                                                                                      Jormakka M,
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Pred. No. 1.8e+06;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              The invention comprises a method for treating a neurological disease or a central nervous system (CNS) disorder. The method involves displaying a therapeutic molecule capable of treating the neurological disease or CNS disorder on a viral display vehicle. The viral display vehicle is then introduced into the olfactory system of a subject to treat the disease or disorder. The method of the invention is useful for preventing, treating and diagnosing neurological diseases or CNS disorders, such as:

Alzheimer's disease; Creutzfeld-Jakob disease; Huntington's chorea; viral
                                                                                                                                                                                                                     Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treating or diagnosing neurological diseases of the central nervous system, e.g. Alzheimer's disease, comprises displaying a polypeptide or diagnostic agent on viral display vehicle and introducing or detecting the display vehicle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Solomon B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-SEP-2002
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                                                                                                                                                                                                                                                                           infections of the brain; brain tumours; lysosomal storage diseases; Parkinson's disease; and multiple sclerosis. The present amino acid sequence represents a peptide which was used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2001; 2001US-00808037.
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                                                                                                          Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIY RAMOT APPLIED RES & IND DEV LTD. MCINNIS P.
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                                                                                                                                     88.6%;
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85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214pp; English.
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1; Mismatches
                                                                                                          Score 39; DB Pred. No. 1.8e
1; Mismatches
                                                                                                 DB 6; Lc..
1.8e+06;
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0;
                                                                                                                                                                Length 9;
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RESULT

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RESULT 11 AAE37229

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AAE37229 standard; peptide; 9 AA

AAE37229;

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ABP55547
ID ABP5
XX ABP5
XX T19-F
XX Stre
XX Hepa
XX Hepa
XX WW020
XX 31-C
XX 31-C
XX 31-C
XX Synt
XX W020
XX ABP5
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                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a Leviminant CC a nucleotide sequence encoding a protein having an avian lysozyme leader CC peptide, or its functional equivalent, joined to a Hepatitis C virus CC (HCV) envelope protein or its part. Also described: (1) a vector CC comprising the recombinant nucleic acid; (2) a host cell comprising the CC recombinant nucleic acid or the vector; and (3) a method for producing CC the host cell with the recombinant nucleic acid or with the vector, where CC the host cell is capable of expressing the protein cited above. (1) has CC hepatotropic, virucide and antiinflammatory activities, and can be used in gene therapy and vaccines. The recombinant nucleic acid is useful for CC cells, such as yeast cells. The HCV envelope proteins in eukaryotic cells, such as yeast cells. The HCV envelope proteins may be used as a CC vaccine, or for incorporation into an immunoassay for the detection of CC anti-HCV antibodies, and/or genotyping of HCV, for prognosing or used is used for producing HCV envelope protein or has cell. ABQ84197
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                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant nucleic acids for expressing Hepatitis C virus (HCV) envelope proteins in eukaryotic cells, comprising a sequence encoding protein having an avian lysozyme leader peptide joined to the HCV envelope protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus; HCV; envelope protein; hepatotropic; virucide; antiinflammatory; gene therapy; vaccine.
                                                                                                                                                                                                                                                             Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                       monitoring of HCV disease, or as a therapeutic agent. The method for producing HCV envelope protein or its part in a host cell. At to AB95528 represent sequences used in exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 303; 319pp; English.
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17-JUL-2001; 2001US-0305604P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a recombinant nucleic acid (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
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                                                             2 XHPQFGG 8
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RHPQFGG
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                                                                                                                              Conservative
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                                                                                                                                                             88.6%;
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                                                                                                                           1;
                                                                                                                                                         Score 39; DB 6;
Pred. No. 1.8e+06;
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                                                                                                                                  Mismatches
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RESULT 12
AAE32860
ID AAE32
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XX AAE32
XX 24-MA
XX Strep
XX Hepat
KW immur
XX Synth
XX Synth
XX Synth
XX 31-OC
XX AAE32
AAAAA
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                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for isolating mRNA from a population of cells. The method involves selectively isolating ribosomes or proteins that bind mRNA in a cell type specific manner and then isolating the mRNA bound to the ribosomes or proteins that bind mRNA. The method is useful for facilitating the analysis and quantification of gene expression in a selected cell type present within a heterogeneous cell mixture. The method may also be used in diagnostics or therapies for human diseases. The present sequence is Strep-tag peptide. This sequence is used to illustrate the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolating cell-type specific mRNAs, useful in gene expression analysis quantification in a specific cell in a heterogeneous cell mixture, by isolating mRNA bound to ribosomes or proteins that bind mRNA in a cell type specific manner.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-2001; 2001US-0340689P.
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9
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                                                                                                                                                                    Streptag peptide.
                                                                                                                                                                                                                            AAE32860;
                                                                                                                                                                                                                                                   AAE32860 standard; peptide; 9
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                                                                                                      Synthetic
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24-APR-2001; 2001EP-00870088
                          24-APR-2002; 2002WO-BE000064.
                                                     31-OCT-2002
                                                                             WO200286101-A2
                                                                                                                                Hepatitis C virus; HCV; envelope protein; virucide; immunostimulant; immune response; T-cell; therapy; infection; pharmaceutical; vaccine
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                             2 XHPQFGG 8
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ilarity 85.7%;
Conservative
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Pred. No. 1.8e
1; Mismatches
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RESULT 13
AAE33270
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Hepatitis C virus (HCV) envelope protein with glycosylation site(s). The HCV envelope protein, or the pharmaceutical composition comprising the envelope protein, is useful as a medicament a vaccine, particularly for inducing a HCV-specific immune response, inducing HCV-specific antibodies or inducing a T-cell function in a mammal. The protein is particularly useful for preventing, treating or diagnosing HCV infection. It is also useful for detecting the presence diagnosing HCV infection. It is also useful for detecting the presence anti-HCV antibodies in a sample. The present sequence is a peptide used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Depla E,
Verheyden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Hepatitis C virus (HCV) envelope protein with N-glycosylation site(s), useful as a vaccine for inducing a HCV-specific immune representation and the specific antibodies, particularly for preventing or treating of the state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 336; 355pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strep epitope tag used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                        Identifying an agent that modulates activity of a membrane-spanning, signal-transducing (MSST) protein, by detecting a conformational change in a MSST protein upon interaction with a ligand.
                                                                                                                                                                                                                                                                                                                                              24-APR-2001;
21-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-2002; 2002WO-US013250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane-spanning signal-transducing
                                                                                                                                                                                            WPI; 2003-103418/09.
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                                                                                                                                                                                                                                                                                               (STRD ) UNIV LELAND STANFORD JUNIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                              Ghanouni P,
                                                                                                                                                                                                                                                                                                                                              2001US-0286250P.
2001US-00935061.
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                                                                                                                                                                                                                                                   Lee TW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; MSST protein; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8e+06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c immune response or treating HCV
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Disclosure;

Page 84; 104pp;

English.

The present invention relates to methods

and

compositions

for identifying

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RESULT 14
ABG72479
ID ABG72
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The invention describes a method of determining the effects of a CC candidate agent on activation of a G protein coupled receptor (GPCR). The CC method comprises contacting a candidate agent with a modified G protein CC alpha subunit and a GPCR, and detecting a level of G protein activation is contacting a ferrivation is contacting a ferrivation is contactive of the effects of the agent on the activity of GPCR. The CC method is useful for determining the effects of a candidate agent on CC activation of a G protein coupled receptor, evaluating new agonists, cc and/or inverse agonists for GPCRs, identifying ligands for GPCRs, and CC developing a strategy for identifying GPCRs involved in different CC biological processes, including diseases. The invention provides rapid cand more sensitive bioassays for evaluating new agonists and/or inverse agonist for GPCRs. The method can be performed using membranes, cc which increases both the ease of performing the assay and its efficacy, and also allows high throughput acreening of GPCR activity. Furthermore, this method directly measures GPCR activity, and thus is less labour-cc intensive than the conventional methods. This sequence represents the Strep tag, an example of an epitope tag that can be used to tether the
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                                                                                                                                                                                                                                                                                                                                                                                                Determining effects of candidate agent on activation of a G protein coupled receptor (GPCR) for evaluating new agonists and/or inverse agonists for GPCRs by contacting a candidate agent with a modified (protein alpha subunit and a GPCR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; alpha sub-unit; G protein coupled receptor; GPCR; protein activation; G protein coupled receptor activation; protein coupled receptor identification; strep tag.
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Pred. No.
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Query Match
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Matches 6; Conserv

Conservative

88.6**%**; 85.7**%**;

Score 39; Pred. No.

Mismatches

1.8e+06; 0;

Indels

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Gaps

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Length

XHPQFGG

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RESULT 15
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Matches
                                  reaction solution containing all necessary components of the transcription/translation system, amino acids, nucleotides and metabolites that supply energy and that are needed for synthesis. The proteins formed are immobilised on a matrix. The method allows simple recovery of proteins without a separate isolation step and the amount of proteins produced can be determined before a reaction is complete. Continuous removal of proteins prevents it interfering with the expression process, making possible synthesis of proteins that interact adversely with the process, so normally produced and is applicable to proteins of any size. This sequence represents a highly conserved peptide from E. coli streptavidin which is used to illustrate the method
                                                                                                                                                                                                                                                                 comprises a matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9 AA;
Sequence
                          peptide from E. coli streptavidin of the invention.
                                                                                                                                                                                                                                       Claim 13;
                                                                                                                                                                                                                                                                             Expressing genes in cell-free system, useful comprises that the protein formed is removed
                                                                                                                                                                                                                                                                                                                                            Erdmann VA, Lamla T,
                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-2001; 2001DE-01037792
                                                                                                                                                                                                                                                                                                                                                                                                                           06-AUG-2001; 2001DE-01037792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell-free transcription system; cell-free translation system;
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                                                                                                                                                                                                           This invention describes a novel method of expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein synthesis;
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                                                                                                                                                                                                                                                                                                                                                                        (ERDM/) ERDMANN V
                                                                                                                                                                                                transcription and translation system which comprises using
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                                                                                                                                                                                                                                                                            for preparation of proteins, from solution by binding to
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Search completed: March 2, 2005, 13:02:45 Job time: 36.0325 secs

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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105.489 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES
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Sequence 30, Appl Sequence 18, Appl	Sequence 75, Appl	Sequence 32, Appl Sequence 166, App	Sequence 14, Appl Sequence 77, Appl	77,	Sequence 3. Appli	3 25	Sequence 1, Appli	Description

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-10-345	US-10-650-585-4	US-10-017-736-4	US-10-449-831A-204	US-10-449-831A-192	US-10-449-831A-198	-80	US-10-345-618-8	US-10-416-708A-64	US-10-416-708A-10	US-10-345-618-13	US-10-345-618-11		US-10-416-290-57	US-10-448-609-8	US-10-422-262-12	US-10-344-607-20	Ļ	-10-344	US-10-342-805-1	-397	US-09-904-599A-8	US-10-771-173-13	8-140-1	US-10-263-230A-12	US-10-060-765-13	US-09-802-154-18	US-09-801-968-18	US-10-494-248-5	-10-753-309-	US-10-397-438A-6	US-10-692-071-3
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## ALIGNMENTS

US-10-026-578B-1 RESULT 1

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                                                                                                                                                                                            US-10-026-578B-1
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Publication No. US20030083474A1
GENERAL INFORMATION:
APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Te
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
COPTWANDE DESCRIPTION OF THE PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                           SOPTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
                                                                                              Matches
                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                               2 XHPQFGG 8
2 RHPQFGG
                                                                                              6
                                                                                              Conservative
                                                                                                                    88.6%;
                                                                                           Score 39; DB 14; Length 8;
Pred. No. 1.3e+06;
1; Mismatches 0; Indels
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PRIOR FILING DATE: 2001-09-26
PRIOR PRIOR APPLICATION NUMBER: JP 227094/2001
PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: JP 6910/2001
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: JP 401417/2000
PRIOR PILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
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US-09-808-037-32
                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
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Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 32
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Patent No. US20020123101A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application UPatent No. US20020052311A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: INOUE, Akio
APPLICANT: SHMMIZU, Yoshihiro
APPLICANT: UEDA, Takuya
IITLE OF INVENTION: Process for Producing Peptides By Using In Vitro
TITLE OF INVENTION: Transcription/Translation System
FILE REFERENCE: 1752-0151p
CURRENT APPLICATION NUMBER: US/09/983,067
CURRENT FILING.DATE: 2001-10-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
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CURRENT FILING DATE: 2001-03-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
OTHER INFORMATION: Strep-tag binding to streptavidin

NAME/KEY: MISC FEATURE
LOCATION: (1)..(9)

OTHER INFORMATION: Schmidt & Skerra, 1993, "The random peptide library-assisted
OTHER INFORMATION: enginerring of a C-terminal affinity peptide, useful for the
OTHER INFORMATION: detection and purification of a functional IgFv fragment",
OTHER INFORMATION: Protein Eng. 6(1):109-122.
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APPLICANT: HANAN, Eilat
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Pred. No. 1.3e+06;
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APPLICANT: Ghanouni, Pejman

APPLICANT: Lee, Tae Weon

TITLE OF INVENTION: Conformational assays to detect binding

TITLE OF INVENTION: to G protein-coupled receptors

FILE REFERENCE: STAN213

CURRENT APPLICATION NUMBER: US/09/935,061

CURRENT FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 60/286,250

PRIOR APPLICATION NUMBER: 60/286,250

PRIOR FILING DATE: 2001-04-24

NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
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US-10-128-590-77
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                                       Query Match
Best Local Similarity 85.,
Thes 6; Conservative
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TITLE OF INVENTION: Core-glycosylated HCV envelope proteins
FILE REFERENCE: 135 PCT
CURRENT APPLICATION NUMBER: US/10/128,590
CURRENT FILING DATE: 2002-07-22
NUMBER: PSEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 77
LENGTH: 9
                                                                                                                                                                                                                                                                                                                                              Sequence 77, Application US/10128590 Publication No. US20030108561A1 GENERAL INFORMATION:
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Best Local Similarity
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Best Local
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                                2 XHPQFGG
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85.7%;
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                                                                                 Score 39; DB 14;
Pred. No. 1.3e+06;
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Pred. No. 1.3e+06;
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RESULT 6
US-10-345-618-14
; Sequence 14, Application US/10345618

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RESULT 8
US-10-394-788-32
IS-quence 32, Application US/10384788
Publication No. US20040013647A1
Publication No. US20040013647A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SOLOMON, Beka
APPLICANT: FRENCEL, Dan
FILE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A PLAQUE-FORMING DISEASE
FILE REFERENCE: SOLOMON-2D. 2
FILE REFERENCE: SOLOMON-2D. 2
CURRENT APPLICATION UNMER: US/10/384,788
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: streptag
US-10-128-587A-77
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CURRENT APPLICATION NUMBER: US/10/128,587A
CURRENT FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 98
SOFTWARE: Patentin version 3.1
SEQ ID NO 77
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/345,618
CURRENT FILING DATE: 2003-01-16
PRIOR APPLICATION NUMBER: US/09/509,031
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
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APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Constructs and methods for expression of recombinant HCV envelops
TITLE OF INVENTION: proteins
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APPLICATION NUMBER:
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85.7%; Pred. No. 1.3e+06;
tive 1; Mismatches 0
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RESULT 10
US-10-425-000-75
US-10-425-000-75
(Sequence 75, Application US/10425000
(Publication No. US20040052777A1
(GENERAL INFORMATION:

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NUMBER OF SEQ ID NOS: 237
SOFTWARE: Patentin version 3.2
SEQ ID NO 166
LENGTH: OJATE: 2003-05-31
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PRIOR FILING DATE: 1999-12-29
PRIOR PELICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/152,417
PRIOR APPLICATION NUMBER: 60/152,417
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: PCT/IL00/00518
PRIOR FILING DATE: 2000-08-31
NUMBER OF SEQ ID NOS: 33
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Best Local Similarity
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Best Local Similarity
APPLICANT: Nesbit, Mark
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Kringle Polypeptides
TITLE OF INVENTION: Angiogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Koentgen, Frank
TITLE OF INVENTION: Higher molecular weight entities and uses therefor
FILE REFERENCE: 2385978
CURRENT APPLICATION NUMBER: US/10/449,831A
CURRENT FILING DATE: 2003-05-30
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PRIOR APPLICATION NUMBER: 09/808,037
PRIOR FILING DATE: 2001-03-15
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PRIOR APPLICATION NUMBER: 10/162,889
PRIOR FILING DATE: 2002-06-06
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PRIOR APPLICATION NUMBER: 09/830,954
                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Strep tag
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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Pred. No. 1.3e+06;
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Pred. No.
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                          and Methods
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                          to Inhibit
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RESULT 12
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                                                                              GENERAL INFORMATION:
APPLICANT: Murray, Clare Margaret
APPLICANT: Hutchinson, Raymond
APPLICANT: Bantick, John Raymond
APPLICANT: Sullivan, Michael
APPLICANT: Donald, David Keith
APPLICANT: Donald, David Keith
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 6
                                                                                                                                                                                                        Sequence 30, Application US/10272196 Publication No. US20040072746A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application Publication No. US2004005 GENERAL INFORMATION: APPLICANT: Nesbit, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.2 SEQ ID NO 75
                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 10/233,675
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Description: 2002-09-04
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Best Local
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OTHER INFORMATION: Purification tag
:-10-425-000-75
                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding
TITLE OF INVENTION: Using Them to Inhibit Anglogenesis
FILE REFERENCE: STOLOGY-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 10/233,675
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ ID NOS: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/424,999
CURRENT FILING DATE: 2003-04-29
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ORGANISM: Artificial Sequence
FEATURE:
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                                                    Jackson, Andrew Paul
Jackson, Clive Geoffrey
                                     Cook,
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Vo. US20040052810A1
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k, Ian David
ION: INHIBITORS OF MONOCARBOXYLATE TRANSPORT
06275-285001
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85.7%; Pred. No. 1.3e+06;
tive 1; Mismatches 0; Indels
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85.7%; Pred. No.
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1.3e+06;
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GENERAL INFORMATION:

APPLICANT: Kobilka, Brian K.

APPLICANT: Ghanouni, Pejman

APPLICANT: Lee, Tae Weon

TITLE OF INVENTION: Conformational assays to detect binding

TITLE OF INVENTION: to membrane spanning, signal-transducing I

FILE REFERENCE: STAN-213CIP

CURRENT APPLICATION NUMBER: US/10/692,071

CURRENT FILING DATE: 2003-10-22

PRIOR APPLICATION NUMBER: DT/US02/13250

PRIOR APPLICATION NUMBER: 09/935,061
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US-10-692-071-3
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US-10-612-410-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/396,627
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/417,172
PRIOR FILING DATE: 2002-10-10
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30

LENGTH: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods and Compositions for the Production, Identification and TITLE OF INVENTION: Purification of Fusion Proteins FILE REFERENCE: 0942.551003 CURRENT APPLICATION NUMBER: US/10/612,410 CURRENT FILING DATE: 2003-07-03 PRIOR APPLICATION NUMBER: 60/333,756 PRIOR APPLICATION NUMBER: 60/333,756 PRIOR FILING DATE: 2002-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/272,196
CURRENT FILING DATE: 2002-10-16
PRIOR APPLICATION NUMBER: US 60/329,318
PRIOR FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bennett, Robert P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Strep epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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85.7%;
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Pred. No. 1.3e+06;
1; Mismatches 0
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Pred. No. 1.3e+06;
                                                                                                                                signal-transducing proteins
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Page 5
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Sequence 6, Application US/10397438A
Publication No. US20040191869A1
GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn AB
TITLE OF INVENTION: Pusion vectors
FILE REFERENCE: 00126
CURRENT APPLICATION NUMBER: US/10/397,438A
CURRENT FILIND DATE: 2002-11-05
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Strep-tag
US-10-397-438A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 60/286,250
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 3
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: epitope tag peptide
US-10-692-071-3
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Search completed: March Job time: 25.878 secs
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US-10-397-438A-6
                                                                                                                                                              Query Match 88.6%; Score 39; DB 16; Length 9; Best Local Similarity 85.7%; Pred. No. 1.3e+06; Matches 6; Conservative 1; Mismatches 0; Indels
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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length: 2000000000
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Match Length
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1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgm2_6/ptodata/1/iaa/6B_COMB.pep:*

6: /cgm2_6/ptodata/1/iaa/backfIles1.pep:*
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GenCore version 5.1.6
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                 US-08-660-626-3
US-08-948-097-1
US-08-948-097-1
US-09-031-168-3
US-09-160-567-14
US-09-672-239-3
US-09-672-239-3
US-09-69-516-3
US-09-69-516-51
US-08-397-020-6
US-08-897-020-6
US-08-897-020-6
US-08-897-020-6
US-08-897-020-6
US-08-897-020-6
US-08-13-1024-11
US-09-640-041-7
PCT-US95-1024-11
US-08-664-444-3
US-08-664-444-3
US-08-664-444-3
US-08-68-444-3
US-08-68-68-444-3
US-08-68-444-3
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39 88.6 178 4 US-09-710-299-13 39 88.6 178 4 US-09-509-031-13 39 88.6 179 3 US-08-897-020-7 39 88.6 197 3 US-08-823-7 39 88.6 198 3 US-08-828-741B-8 39 88.6 198 4 US-09-509-031-8 39 88.6 198 4 US-09-710-299-8 39 88.6 334 4 US-09-710-299-6 39 88.6 342 3 US-08-828-741B-6 39 88.6 342 3 US-08-828-741B-6 39 88.6 342 4 US-09-710-299-6 39 88.6 342 4 US-09-710-299-6 39 88.6 342 4 US-09-710-799-6 39 88.6 342 4 US-09-707-77-740-7305 39 88.6 487 4 US-09-777-77-74305	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	2
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	495	487	409	386	342	342	342	342	334	198	198	198	198	197	197	178	178	7 / K
US-09-710-299-13 US-09-509-031-13 US-09-509-031-13 US-09-509-031-13 US-08-820-7 US-08-828-741B-8 US-09-160-567-8 US-09-710-299-8 US-09-710-299-6 US-09-710-299-6 US-09-710-299-6 US-09-710-299-6 US-09-710-299-6 US-09-710-299-6 US-09-710-77-77-78-43055 US-09-770-777-743055	w	4	4.	ω	4	4.	w	w	4	4	4	w	w	w	ω	4.	4	L
	US-08-828-741B-4				US-09-509-031-6	-09-710-299-	-09-160-567-			-09-509-031-						9-09		
	4	430	2			6	6	6	4	8	8	9	8	7,	7,	13,	13,	Į,
=	Appli	43055, A	Appli	Appli	Appli	Appli	Appli	Appli	Appli	App1i	Appli	Appli	Appli	App1 i	App1i	App1	App1	يارك

## ALIGNMENTS

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Sequence 3, Application US/08660626

Patent No. 5789655

GENERAL INFORMATION:

APPLICANT: Stanley B. Prusiner

APPLICANT: Glenn C. Telling

APPLICANT: Fred E. Cohen

APPLICANT: Michael R. Scott

TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING

TITLE OF INVENTION: EPTOPE-TAGGED PROTEINS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
몽
                                                                                                                                                      US-08-660-626-3
                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Valeta Gregg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 0753
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                          TELEPHONE: (415) 322-5070
TELEPAX: (415) 854-0895
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCIII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,626
                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2200 Sand
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                    2 XHPQFGG 8
                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3E: Fish & Richardson 2200 Sand Hill Road,
                                                                                            88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/660,626
                                                                                                                                                                                                                                                                                                                                                07532/003001
                                                                          1; Mismatches
                                                                                            Score 39; DB 1;
Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suite 100
                                                                          <u>,</u>
                                                                                                              Length 9;
                                                                          Indels
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Gaps

<u>,,</u>

US-08-828-741B-14

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APPLICANT: Skerra, Arne
APPLICANT: Skerra, Arne
APPLICANT: VOSB, Selma
TITLE OF INVENTION: Streptavidin Muteins
FILE REFERENCE: HUBR 1119
CURRENT APPLICATION NUMBER: US/08/948,097C
CURRENT FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: DE 196 41 876.3
EARLIER FILING DATE: 1996-10-10
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-08-828-741B-14
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                                                                                                                                                                                                                              RESULT 3
US-08-948-097-1
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                          Sequence 1, Application US/08948097C
           SEQ ID NO 1
LENGTH: 9
                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: DIGIGIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Koentgen,
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New Vor'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                            3 RHPQFGG 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 amino acids
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                      88.6%;
                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 3;
Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
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RESULT 5 US-09-160-567-14 ; Sequence 14, A

Application US/09160567

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                                                                                                                         ; MOLECULE TYPE: peptide US-09-031-168-3
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Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                            Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: ASCILI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,168
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Stanle:
APPLICANT: Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: BINDING
OTHER INFORMATION: Binding ligand for streptavidin
                                                                                                                                                                                                                        TELEFAX: (415) 854-0875
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Valeta Greeg
REGISTRATION NUMBER: 35,127
REFERENCE/DOCKET NUMBER: 0753
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 322-5070
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: TRANSGENIC ANIMALS EXPRESSING TITLE OF INVENTION: EPITOPE-TAGGED PROTEINS
                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                             Local Similarity
les 6; Conserv
                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 XHPQFGG 8
                                2 XHPQFGG
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                                                                                                                                                            amino acid
GY: linear
 RHPQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stanley B. Prusiner Glenn C. Telling Fred E. Cohen Michael R. Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Fish & Richardson
2200 Sand Hill Road, Suite 100
                                                                                                                                                                                           9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                  Conservative
                                                                                85.7%;
                                                                                                                                                                                                                                                                                                                                                                            08/660,626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 3; Length 9;
Pred. No. 4.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                              07532/003001
                                                                                Score 39; DB 3;
Pred. No. 4.1e+05;
                                                                    Mismatches
                                                                                                   Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                        Gaps
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FILE REPERENCE: STAN-204
CURRENT APPLICATION NUMBER: US/09/672,239
CURRENT FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 9
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear;

MOLECULE TYPE: DNA (genomic)
US-09-160-567-14
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                                                                                                                                                                                                                                                                 Sequence 3, Application US/09672239
Patent No. 6448377
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 85.
Matches 6; Conservative
ORGANISM: Homo sapiens
                                                                                                                                                                          APPLICANT: Lee, Tae Weon
APPLICANT: Kobilka, Brian
TITLE OF INVENTION: MODIFIED G PROTEIN SUBUNITS
FILE REFERENCE: STAN-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
APPLICANT: Treutlein, Herbert R.
APPLICANT: TRAILIGIN, CATALYTIC ANTIBODIES AND A METHOD TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPHAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: gir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11530
                                                                                                     FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                    RHPQFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        XHPQFGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.6%; Score 39; DB 3;
85.7%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 8
US-09-509-031-14
; Sequence 14, Application US/09509031
; Patent No. 6590080
; GENERAL INFORMATION:
; APPLICANT: Koentgen, Frank
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US-09-710-299-14
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Patent No. 6521741
GENERAL INFORMATION:
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/710,299
APPLICATION NUMBER: US/09/710,299
FILING DATE: 09-No. 6521741-2000
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE: -UNKNOWN>
FILING DATE: -UNKNOWN>
FILING DATE: -UNKNOWN>
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tarlinton, David M.
Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Koentgen, Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                   2 XHPQFGG 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 XHPQFGG 8
                                                                                                                                                                                                                                         6;
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                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09710299
                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suess, Gabriele M.
                                                                                                                                                                                                                                       88.6%; Score 39; DB 4;
85.7%; Pred. No. 4.1e+05;
tive 1; Mismatches 0
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85.7%;
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1; Mismatches
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US-09-669-516C-3
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RESULT 10
US-08-294-386C-11
; Sequence 11, Application US/08294386C
; Patent No. 5646030
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                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Strep peptide US-09-669-516C-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/031,168
PRIOR FILING DATE: 1998-02-26
PRIOR PELIVATION NUMBER: 08/660,626
PRIOR FILING DATE: 1996-06-06
PRIOR PELIVATION NUMBER: 08/521,992
PRIOR PILING DATE: 1995-08-31
PRIOR PELIVATION NUMBER: 08/509,261
PRIOR PILING DATE: 1995-07-31
PRIOR PILING DATE: 1995-07-31
PRIOR APPLICATION NUMBER: 08/242,188
PRIOR APPLICATION NUMBER: 08/242,188
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CURRENT FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09669516C Patent No. 6602672
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Best Local
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Best Local (
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                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Prusiner, Stanley B.
APPLICANT: Telling, Glenn C.
APPLICANT: Telling, Glenn C.
APPLICANT: Cohen, Fred E.
APPLICANT: Scott, Michael R.
TITLE OF INVENTION: RECOMBINANT CONSTRUCT ENCODING EPITOPE
TITLE OF INVENTION: TAGGED PrP PROTEIN
FILE REFERENCE: UCAL-045CON
CURRENT APPLICATION NUMBER: US/09/669,516C
CURRENT FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBOIDES AND A METHOD OF PRODUCING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
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                                                                                                                                                                                                                  88.6%; Score 39; DB 4; Length 9; 85.7%; Pred. No. 4.1e+05;
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Pred. No. 4.1e+05
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RESULT 11
US-08-737-316A-5
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/294,386C
FILING DATE: AUGUST 23, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: SYZZ-010CIP
TELECOMMUNICATION INFORMATION:
TELESPHONE: 617/330-1310
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SKERRA, A
APPLICANT: WARDENBER
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08737316A Patent No. 5849576
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Ray, E
         COUNTRY: U.S.A.
ZIP: 2005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHOIN DATA:
APPLICATION NUMBER: US/08/737,316A
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APPLICANT: Lin, Edmund C.C.
APPLICANT: Crea, Roberto
TITLE OF INVENTION: Method Of Isolating Mutant Cells
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
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HYPOTHETICAL:
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                             CITY: Washington STATE: D.C.
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200 State Street
                                                                                                                                                                                                               BE: Nikaido, Marmelstein, Murray & Oram LLP
655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
                                                                                                                                                                                                                                                                               SKERRA, Arne
WARDENBERG, Christina
WARDENBERG, Christina
VENTION: USE OF THE TETRACYCLINE PROMOTER FOR THE
VENTION: STRINGENTLY REGULATED PRODUCTION OF RECOMBINANT PROTEINS IN
VENTION: CELLS
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MBER: US/08/737,316A
12-NOV-1996
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Pred. No. 0.66;
                                                   Version #1.30
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RESULT 12
US-08-897-020-6
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Best Local (
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                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P-91,242
APPLICATION NUMBER: P-91,242
FILING DATE: 19-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Huw R. Jones
REGISTRATION NUMBER: 33, 916
REFERENCE/DOCKET NUMBER: WH5020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2317
TELEPHONE: (203) 812-2317
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: PCT/EP
FILING DATE: 17-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: DE P 4.
APPLICATION UNMBER: DE P 4.
ATTORNEY/AGENT INFORMATION:
NAME: Kitch, Monica C.
REGISTRATION NUMBER: 36,10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202)638-4810
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                TELEFAX: (203) 812-5492 INFORMATION FOR SEQ ID NO:
                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYBE: Diskette, 3.5 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS v. 6.30 SOFTWARE: Word for Windows 6.0 CURRENT APPLICATION DATA: APPLICATION UMBER: US/08/897,020 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shanafelt, Armen; Greve, Jeffrey; Roczniak, Steven TITLE OF INVENTION: High-affinity Interleukin-4 Muteins NUMBER OF SHQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
   MOLECULE TYPE:
DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CITY: West Haven
STATE: CT
                                      STRANDEDNESS:
TOPOLOGY: 11
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                                                                         TYPE: amino acid
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Similarity 85.7%;
6; Conservative
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400 Morgan Lane
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peptide
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Pred. No. 0.66;
1; Mismatches
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                                                                                                               US-08-895-707-11
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Best Local Similarity
Matches 6; Conserv
                                                    Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/895,707
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wootton, Thomas A.
REGISTRATION NUMBER: 35,004
REFERENCE/DOCKET NUMBER: 6054
                                                                                                                                                                                                                                                            TELEFAX: 616-833-8897
INFORMATION FOR SEQ ID NO:
                                                                                                                                                       TOPOLOGY: 11Hear
MOLECULE TYPE: Pep
MOLECULE TYPE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Rel. #1.0, Ver.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Evans, David B.
TITLE OF INVENTION: Special Constructs and Complexes of
TITLE OF INVENTION: Cyclin E
                                                                                                                             ANTI-SENSE: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 616-833-7914
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RHPQFGG 10
                         XHPQFGG 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 Henrietta Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Pharmacia & Upjohn, Co.) alternatively, for U.S. filing: Hollingsworth, Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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Sharma, Satish K.
                                                       Conservative
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                                                                     88.6%;
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85.7%;
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                                                                     Score 39; I
Pred. No. 0.
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RESULT 14 US-09-350-823-6

; Sequence 6, Application US/09350823

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Patent No. 6313272

GENERAL INFORMATION:
APPLICANT: Shanafelt, Armen; Greve, Jeffrey; Roczniak, Steven APPLICANT: Shanafelt, High-affinity Interleukin-4 Muteins TITLE OF INVENTION: 9

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Bayer Corporation, Pharmaceutical Division STREET: 400 Morgan Lane CITY: West Haven

STATE: CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-350-823-6
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                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-715-805-13
                                                                                                   APPLICANT: Itch, No. 6716626uyuki
APPLICANT: Kavanaugh, W. Michael
TITLE OF INVENTION: PRODUCTS
TITLE REFERENCE: PP-16758.001/201130.408
FILE REFERENCE: PP-16758.001/201130.408
FILE REFERENCE: PP-16758.001/201130.408
FURRENT APPLICATION NUMBER: US/09/715,805
CURRENT FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09715805
Patent No. 6716626
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
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MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS v. 6.30
SOFTWARE: Word for Windows 6.0
CURRINT APPLICATION UNMEER: US/09/350,823
PILING DATE: 09-Jul-199
CLASSIFICATION UNMEER: US/09/350,823
PILING DATE: 09-Jul-199
CLASSIFICATION NUMBER: 08/897,020
PILING DATE: CUNKNOWN>
PRIOR APPLICATION NUMBER: 33,916
REPLICATION NUMBER: 33,916
REGISTRATION NUMBER: 33,916
REGRENCE/DOCKET NUMBER: WH5020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 812-2492
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE, CHARACTERISTICS:
FUNDTH: 10
                                                                     TYPE: PRT
ORGANISM: Unknown FEATURE: OTHER INFORMATION: Residues which bind to paramagnetic streptavidin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match
Local Similarity 85.7%;
hes 6; Conservative 1
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MOLECULE TYPE: peptide
DESCRIPTION: tag for streptavidin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: no
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STRANDEDNESS: single
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Pred. No. 0.66;
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; OTHER INFORMATION: beads (used for purification).
US-09-715-805-13

Query Match
Best Local Similarity 85.7%; Pred. No. 0.66;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps

Qy 2 XHPOFGG 8
| | | | | | | |
Db 4 RHPOFGG 10

Search completed: March 2, 2005, 12:25:34

Job time: 9.10569 secs
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Minimum
Maximum
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No.
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Perfect score:
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Maximum Match 100%
Listing first 45 s
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: pir2:*
3: pir3:*
4: pir4:*
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DnaJ protein XF223
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A,Molecule type: DNA
A,Residues: 1-332 <KUR>
A,Residues: 1-332 <KUR>
A,Cross-references: UNIPROT:Q8YIM3; GB:AE008917; PIDN:AAL51601.1; PID:g17982326; GSPDB:(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75436
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dc, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zale, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodu A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75436
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G75436
A; Gene: BMEI0420
A; Map position:
                                                                                                                                                                                                                     C;Accession: AF3304
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AP3304
                                                                                                                                                                                                                                                                                                                                                                                                                    oxidoreductase (BC 1.1.1.-) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-20
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C;Superfamily: Escherichia coli yceA protein
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A;Residues: 1-300 <WHI>
A;Cross-references: UNIPROT:Q9RVC9; GB:AE001960; GB:AE000513; NID:g6458833; PIDN:AAF106;
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: DR1100
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Best Local S
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Pred. No.
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T.; Zalewski, C.; Ma
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RESULT 5
A82547
hypothetical constraints
C;Species: Xy
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A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: B71073
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                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Y1031 - Yersinia pestis plasmid pMT1
C;Species: Yersinia pestis
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Kawarabayasi, Y
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                                                                                                                                                                                                                                             A;Gene: Y:
A;Genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-360 <KAW>
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                                                                                                                                                                                                                                                                                                               A;Residues:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
                                                                                                                                                                                                                                                                                                                                                                                                                   nfect. Immun.
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Best Local S
Matches 5
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Best Local S
Matches 5
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;Species: Pyrococcus horikoshii
;Date: 14-Aug_1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                             ;Lindler, L.E.; Plano, G.V.; Burland, V.; Mayhew, G.F.; Blattner, F.R.
nfect. Immun. 66, 5731-5742, 1998
;Title: Complete DNA sequence and detailed analysis of the Yersinia pestis KIM5
;Reference number: Z18268; MUID:99043898; PMID:9826348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; nucleic acid sequence not shown; translation
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                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:068740; EMBL:AF074611; NID:g3883003; PID:g3883032; PIDN:AAC
                                                                                                                                                                                                                                                                                                                                             Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                             Genetics:
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     al protein XF2515 [imported] -
Xylella fastidiosa
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6; Conserva
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5; Conserv
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Y.; Funahashi,
                                                                                                                                                                           Similarity 5; Conserv
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24;
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                          (strain 9a5c)
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A,Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigr J.D.; Junqueira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. C.; Miyaki, C.Y., A; Mathors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A., F.G.; Nunes, L.R.; Oliveira, M.A.; de Rosa JT., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak R; Asuthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva, J.W.A.; da Silveira, M.F.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Editore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Editore, A.L.; Za, R.G.; Editore, A.L.; Za, R.G.; Editore, A.L.; Za, R.G.; M.S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Za, R.G.; Santelli, R.Y.;
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R;anonymous, The Xylella i
Nature 406, 151-157, 2000
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C;Genetics:
A;Gene: XF2515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein SCH35.17 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change C;Accession: 736642 C;Accession: 736642 D.; Bentley, S.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, June 1999
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A;Experimental source: strain 9a5c
hypothetical protein alr7551 [imported] - Nostoc sp. (strain PCC C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-189 <OLI>
A;Cross-references: UNIPROT: 09X8Y9;
A;Experimental source: strain A3(2)
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A; Accession: T36642
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Best Local
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5; Conserva
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Pred. No.
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Pred. No. 12;
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          strain PCC 7120
09-Jul-2004
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A;Molecule type: mRNA
A;Residues: 21-437 <ANK1>
A;Crose-references: UNIPROT:P14885; EMBL:X13319; NID:g64715; PIDN:CAA31694.1; PID:g6471
A;Accession: B31142
                                                                                                                                                                                            gelsolin, ovarian - African clawed frog (fragments)
C;Species: Kenopus laevis (African clawed frog)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A31142; B31142
R;Ankenbauer, T.; Kleinschmidt, J.A.; Vandekerckhove, J.; Franke, W.W.
J. Cell Biol. 107, 1489-1498, 1988
A;Title: Proteins regulating actin assembly in oogenesis and early embryoge
A;Reference number: A31142; MUID:89008590; PMID:2844829
A;Accession: A31142;
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R;anonymous, Gendscope
Rubmitted to the EMBL Data Library, July 1999
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                                                                A; Molecule type: protein A; Residues: 1-20 < ANK2>
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: H75,31
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2533
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A; Residues: 1-362 < KAW>
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A; Residues: 1-213 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Cross-referencas: UNIPROT:Q9V0D5; GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB4976;Experimental source: strain Orsay
                                           Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: malate dehydrogenase ylbC
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Best Local Similarity
Matches 5; Conserv
                  Superfamily: gelsolin, gelsolin repeat homology Keywords: actin binding
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repeat homology (fragment) <GEL1>
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62.5%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.
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No.
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                                                                                                                                                                                                                                          embryogenesis
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                                           RESULT 12
T00484
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C;ACCEBELOW. C;ACCEBELOW. C;ACCEBELOW. C;CACCEBELOW. C;CACCEBELOW. C;Takami, H.; Nakasone, K.; Takakı, ..., ...
R;Takami, H.; Nakasone, K.; Takakı, ..., ...
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium
A;Title: Complete genome sequence of the alkaliphilic bacterium
A;Title: Complete genome sequence of the alkaliphilic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola (Species: Prevotella ruminicola (Species: Prevotella ruminicola (C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 (Accession: T10487 R;Wen, Z.T.; Morrison, M. submitted to the EMBL Data Library, December 1996 A;Reference number: Z17049 A;Accession: T10487
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                                                                                                                                      A;Gene: BH3873
C;Superfamily:
                                                                                                                                                                         A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                  acetolactate synthase large subunit BH3873 [imported] - Bacillus halodurans (strain C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 16-Aug-2004
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C;Superfamily: glutamate dehydrogenase (NAD(P)+)
C;Keywords: NADP; oxidoreductase
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A; Residues: 1-444 <WEN>
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                                                                                                                                                                                                                                                                                                                                                                    C; Accession: A84134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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A;Experimental source: strain B14
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Best Local S
Matches 5
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Best Local S
Matches 5
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Best Local S
Matches 5
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les 5; Conserv
470
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                                                                   Similarity
5; Conserv
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RTHPRFEQ 477
                                  RXHPQFEK 8
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                                                                                                                                      Acetolactate synthase, large subunit/pyruvate oxidase
                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                  K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji,
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Pred. No. 72;
2; Mismatches
                                                                                   Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
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                                                                     Mismatches
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                                                                                                     DB 2;
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                                                                                                     Length 543
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                                                                     Indels
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and Hira C-12

hypothetical protein At2g35030 [imported] - Arabidopsis N;Alternate names: hypothetical protein F19I3.26

thaliana

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A;Residues: 1-1473 <PEA>
A;Residues: 1-1473 <PEA>
A;Cross-references: UNIFROT:014167; EMBL:Z98560; PIDN:CAB11176.1; GSPDB:GN00066; SPDB:SFA;Cross-references: UNIFROT:014167; cosmid c4C5
A;Experimental source: strain 972h-; cosmid c4C5
R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, November 1997
A;Reference number: Z21719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ferredoxin oxidoreductase SPAC4C5.05c - fission yeast (Schizosacch. C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T38791; T37495 R;Pearson, D.; Churcher, C.M.; Barrell, B.G.; Rajandream Wood, V. submitted to the EMBL Data Library, August 1997
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T38791
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A;Experimental source: Cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
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A;Description: Arabidopsis thaliana chromosome II BAC F1913 genomic sequence.
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A;Accession: G84763
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R; Rounsley, S.D.; Lin, X.;
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A; Residues: 1-627 <STO>
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A;Accession: T00484
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A; Residues: 1-755 < CON>
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Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                Cross-references: EMBL:AL009197; PIDN:CAA15714.1; GSPDB:GN00066; SPDB:SPAC10F6.01c
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Best Local
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Best Local
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   1221 RDHPQFIK 1228
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P26046; GB:M57425; GB:J05604; NID:g169183; PIDN:AAA63415.1; C;Comment: This multifunctional enzyme catalyzes the formation of alpha-aminoadipyl-cyst rying out the polymerization steps to form the tripeptide, which is the first common int
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: pcbAB
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A; Residues: 1-3791 < DIE>
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R;Diez, B.; Gutierez, S.; Barredo, J.L.; van Solingen, P.; van der Voort, L.H.M.; Marti
J. Biol. Chem. 265, 16358-16365, 1990
A;Title: The cluster of penicillin biosynthetic genes. Identification and characterizati
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phosphopantetheine

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A;Gene: pCbAB
A;Gene: pCbAB
C;Superfamily: non-ribosomal peptide synthetase; acetate-CoA ligase homology; (C;Superfamily: non-ribosomal peptide synthetase; duplication; ligase; priss-service; protein; cephalosporin biosynthesis; duplication; ligase; priss-service; protein homology caculate; protein homology caculate; priss-service; priss-service; priss-service; protein homology caculate; priss-service; priss
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alpha-aminoadipyl-cysteinyl-valine synthetase (EC 6.-.-.) - Pen N;Alternate names: ACV synthetase C;Species: Penicillium chrysogenum C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change C;Accession: A37886
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A; Residues: 1-3746 <SMI>
A; Residues: 1-3746 <SMI>
A; Comment: This multifunctional enzyme catalyzes the formation of alpha-aminoadipyl-cyst rying out the polymerization steps to form the tripeptide, which is the first common int C; Genetics:
C; Genetics:
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EMBO J. 9, 2743-2750, 1990
A;Title: The multifunctional peptide synthetase performing
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Query Match 90.5%; Best Local Similarity 75.0%; Matches 6; Conservative

Score 38; DB 1; Length 300; Pred. No. 32; 2; Mismatches 0; Indels

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1 Nakamura I., Suzum.
1 Submitted (NOV-2002) to the ...
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3 Submitted (NOV-2002) to the ...
4 Nakamura I., Suzum.
5 Submitted (NOV-2002) to the ...
6 RBL; AB096020; BAC24016.1; -..
6 GO; GO:0004383; F:guanylate cyclase activity; IEA.
6 GO; GO:0006242; P:intracellular signaling cascade; IEA.
6 GO; GO:0007242; P:intracellular signaling cascade; IEA.
7 ThterPro; IPR001054; G cyclase.
7 TherPro; IPR001054; G cyclase.
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Q8CJD2
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Matches 6
                                                                                                                   NAKAMURA I., YAO Y., SUZUKİ N.;
NAKAMURA I., YAO Y., SUZUKİ N.;
NAKAMURA I., YAO Y., SUZUKİ N.;
NAKAMURA I., YAO Y., SUZUKİ N.;
SUDMİLTEĞİ (DEC-2002) to the EMBL/GenBank/DDBJ databaı
EMBL; AB997860; BAC44887.1; -.

RIGGO; GO:0004383; F:SUQANYLATE CYCLASE ACTIVİTY; IEA.
GO; GO:0016829; F:LYASE ACTIVİTY; IEA.
GO; GO:0016829; F:İYASE ACTIVİTY; IEA.
GO; GO:0007242; P:intracellular signaling cascade; II
InterPro; IPR001054; G CYCLASE.

InterPro; IPR001054; G CYCLASE.

InterPro; IPR001080; TERNASN; Ja bind.
Pfam; PF00211; Guanylate CyC; 1.

SVART; SW00044; CYCC; 1.
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01-MAR-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
                                   PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Soluble guanylyl cyclase alpha 2 subunit E219G mutant.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
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Matches 6
PubMed=12368667; DOI=10.1038/nature01095;
Hall N., Pain A., Berriman M., Churcher C., Harris B.,
Mungall K., Bowman S., Atkin R., Baker S., Barron A.,
Buckee C.O., Burrows C., Cherevach I., Chillingworth Chillingworth T., Christodoulou Z., Clark L., Clark R.
Cronin A., Davies R., Davies P., Dear P., Dearden F.,
                                                                                                                                                                                                                                                                                                                                                          Q6LFL4;
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Hypothetical protein. ORFNames=MAL6P1.55, F
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Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases
-i- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry o
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Eukaryota; Metazoa; Arthropoda; He
Eukaryota; Endopterygota; Diptera;
NCBI_TaxID=180454;
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01-MAR-2004 (TrEMBLrel. 26, Las
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01-MAR-2004 (TrEMBLrel. 26, Las
ENSANGPP00000008445 (Fragment).
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                                                                                                                                                                                                      Eukaryota; Alveolata;
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InterPro; IPR001606; ARID.
Pfam; PF01388; ARID; 1.
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HSSP; Q24573; IC20.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Last sequence update)
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Pred. No. 4.5e+02;
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Pred. No. 1.4e+02;
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EMBL; AL109751; CAC09922.1; -.
SEQUENCE 313 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cherevach I., Davis P., Goodhead I., Stevens K., Mungall K., Berriman M., Pain A., Hall N., Atkin R., Chillingworth C., Doggett J., Ormond D., Sanders M., Hayes R., Hall S., Quail M., Barrell B.G; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

EMBL; CR382398; CA2522.1; -

GO; GO:0003998; F:acylphosphatase activity; IEA.

InterPro; IPR001792; Acylphosphatase.

InterPro; IPR001792; Acylphosphatase.
                                                                                                                                                                                                                                                                                                                                                                                                      "A novel tumour associated leucine of gene transcription and splicing. Oncogene 21:3879-3888 (2002).
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Tureci O., Sahin U., Koslowski M., Buss B., Bell C., Ballweber
Zwick C., Eberle T., Zuber M., Villena-Heinsen C., Seitz G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE 2
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C STRAINATCC 49882 / Houston 1;

X PubMed=15210978; DOI=10.1073/pnas.0305659101;

X Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault B.-A., Ard Alsmark U.C.M., Frank A.C., Naeslund A.K., Handley S.A., Huv La Scola B., Holmberg M., Andersson S.G.E.;

The Louse-borne human pathogen Bartonella quintana is a genc derivative of the zoonotic agent Bartonella henselae.";

Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721(2004).

EMBLJ BA897699; CAP27993.1;

EMBLJ BA897699; CAP27993.1;

GO; GO:0016491; F:0xidoreductase activity; IEA.

BR GO; GO:0016118; P:electron transport; IEA.

BR InterPro; IPR000683; GFO/IDH/MocA_C.

Pfam; PF01408; GFO_IDH_MocA_C.

Pfam; PF01408; GFO_IDH_MocA_C; 1.
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Proc. Natl. Acad. Sci. U.S.A. 101:9716-9721 (2004).

EMEL; BX897700; CAF26428.1; -...
GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:00166118; P:electron transport; IEA.
InterPro; IPR001683; GFO/IDH/MocA_N.
InterPro; IPR001683; GFO/IDH/MocA_C.
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STRAIN-TOUIOUSE;
PubMed=15210978; DOI=10.1073/pnas.0305659101;
Alsmark U.C.M., Frank A.C., Karlberg E.O., Legault E
Canbaeck B., Eriksson A.-S., Naeslund A.K., Handley
La Scola B., Holmberg M., Andersson S.G.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bartonella henselae (Rochalimaea henselae).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6G2J1;
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bartonella quintana (Rochalimaea quintana).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobialea;
Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
OrderedLocusNames=BQ09510;
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=38323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
OrderedLocusNames=BH12100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q6G2J1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bartonellaceae; Bartonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01408; GFO_IDH_MocA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35962 MW;
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75.0%;
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Last sequence update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     638383119CD75700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Q8LTT5;
Q8LTT5;
01-OCT-2002 (TrEMBLrel. 22, Li
01-OCT-2003 (TrEMBLrel. 25, Li
01-OCT-2003 (TrEMBLrel. 25, Li
5; to 3; exomuclease-like pro
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SEQUENCE
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STRAIN=1330 / Biovar 1;

MEDLINE=22247741; pubMed=12271122; DOI=10.1073/pnas.192319099;

MEDLINE=22247741; pubMed=12271122; DOI=10.1073/pnas.192319099;

Paulsen I.T. Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

Paulsen I.T. Seshadri R., Nelson K.E., Kalinkac L.M., Beanan M.J.,

Daugherty S.C., DeBoy R. T., Durkin A.S., Kolonay J.F., Madupu R.,

Daugherty S.C., DeBoy R. T., Durkin A.S., Kolonay J.F., Madupu R.,

Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A.,

Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O.,

Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,

Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, 0
01-MAR-2003 (TrEMBLrel. 23, 1
01-JUN-2003 (TrEMBLrel. 24, 1
0xidoreductase, Gfo/Idh/MocA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0016491; F:oxidoreductase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
GO; GO:000618; P:electron transport; IEA.
InterPro; IPR006683; GFO/IDH/MocA_N.
InterPro; IPR004104; GFO_IDH_MocA_C.
Pfam; PF01408; GFO_IDH_MocA, 1.
Pfam; PF01894; GFO_IDH_MocA_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    animal and plant pathogens and symbionts."; proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002). EMBL; AE014453; AAN30507.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=BR1602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=29461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brucella suis.
                                                                         Viruses; dsDNA v
T7-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The Brucella suis genome reveals fundamental similarities between
                                                                                                Vibriophage VpV262.
Viruses; dsDNA viruses,
     SEQUENCE FROM N.A.
                                               NCBI_TaxID=194802;
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6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RXHPQFEK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome.
318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              RXHPOFEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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35582 MW; 7AE81771FF655355 CRC64;
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Last annotation update)
A family.
                                                                                                   RNA stage; Caudovirales; Podoviridae;
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Pred. No.
                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB
Pred. No. 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                               323
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Virology 310:359-371(2003).

EMBL; AY095314; AAM28378.1; -..

EMBL; AY095314; AAM28378.1; -..

EQ; GO:0004527; F:exonuclease activity; IEA.

GO; GO:0004527; F:exonuclease activity; IEA.

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InterPro; IPR008918; 5.3 exo_C.
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STRAIN=16M / ATCC 23456 / Biotype 1;

MEDLINE=20020109, PubMed=11756688; DOI=10.1073/pnas.221575398;

Delvecchio V.G., Kapattal V., Redkar R.J., Patra G., Mujer C., Los T.,

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EMBL, AE009485; AAL51601.1; -.
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NCBI_TaxID=29459;
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MEDLINE-21534947; PubMed=11677608; DOI=10.1038/35101607; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Xrogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
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Q934Z7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salmonella typhi.
Plasmid pHCM2.
Bacteria; Proteobactaria; Gammaproteobacteria;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein HCM2.0069c.
OrderedLocusNames=HCM2.0069c;
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Pfam; PF02615; Ldh 2; 1.

Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid SEQUENCE 360 AA; 39751 MW; 6E9D8B16ECDE6E6F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
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                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CT18;
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Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malate dehydrogenase (EC 1.1.1.37).
Name-mdh; OrderedLocusNames-PH1277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Res. 5:55-76(1998).

CATALYTIC ACTIVITY: (S)-malate + NAD(+) = oxaloacetate + NA SUBUNIT: Homodimer (By similarity).

SUBCELLULAR LOCATION: Cytoplasmic (Probable).

SIMILARITY: Belongs to the LDH2/MDH2 oxidoreductase family.
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Pred. No. 98;
3; Mismatches
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EMBL; AL513384; CAD09936.1; -...
                                                                                                                                                                                                                                          Q65AP7;
Q65AP7;
25-OCT-2004
25-OCT-2004
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Q74YP4;
05-JUL-2004
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            SEQUENCE FROM N.A.

PubMed=15385458;

Golubov A., Neubauer H., Nolting C., Heesemann

"Structural Organization of the pFra Virulence-
Rhamnose-Positive Yersinia pestis.";

Infect. Immun. 72:5613-5621(2004).
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Song Y. Tong Z., Wang L., Han Y.,
Han Y., Pang X., Zhai J., Chen F.,
Ye C., Du Z., Lin W., Wang J., Yu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ
EMBL; AE017045; AAS58659.1; -.
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OrderedLocusNames=pMT024;
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                                                                                                                                                        Bacteria; Proteobacteria;
Enterobacteriaceae; Yersi
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Yersinia pestis.
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Plasmid pMT1
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:eriaceae; Yersinia.
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529 AA; 61
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61074 MW;
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62.5%;
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27,
27,
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                                                                                                                                                                        Gammaproteobacteria;
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Hypothetical protein; Plasmid. SEQUENCE 529 AA; 61074 MW; 9AE89400496940BB CRC64;

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## SUMMARIES

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## ALIGNMENTS

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RESULT 1
AAW59212
01X6XFX3GXGXGXGXGXGXGXGXGXFFFFX8XX02020202020X3X
                                                                                                                  WPI; 1998-218868/20.
                                                                                                                              Skerra A,
                                                                                                                                                      10-OCT-1996;
                                                                                                                                                                  09-OCT-1997;
                                                                                                                                                                                           EP835934-A2
                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                        Streptavidin; ligand; binding affinity; mutant; isolation; purification;
                                                                                                                                                                                                                                     Streptavidin tagged peptide ligand
                                                                                                                                                                                                                                                 27-AUG-1998
                                                                                                                                                                                                                                                                         AAW59212 standard;
                                                                                                                                                                               15-APR-1998.
                                                                                                                                                                                                                                                             AAW59212;
                                                                                                                                          (BIOA-) INST BIOANALYTIK GMBH.
                                                                                                                                                                                                                  recover; immobilise.
                                                                                                                              Voss S;
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Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to isolate, purify or determine fusion proteins including these ligands.

Claim 10; Page 11; 21pp; German.

AAW59211 and AAW59212 are ligands used in a method to assay binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or sensor chips

Sequence 8

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Length 8;

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RESULT 2
AAB35433
ID AAB3
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  Nascent
                                                    23-MAY-2001
                                                                                                   AAB35442;
                                                                                                                                                  AAB35442 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method of detecting nascent proteins involving aminoacylating a tRNA molecule with a 4,4-difluoro-4-bora-3A,4A -diaza-s-indacene (BODIPY) marker leading to the production of a misaminoacylated tRNA. This enables the detection, isolation and analysis of nascent proteins using UV without the usual accompanying radioactivity problems. It may be used to detect mutations, for example in cancer, but the muscular dystrophy, adenomatous polyposis coli and colon cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 47; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-168972/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rothschild Ku,
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25-AUG-1999;
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protein detection method related peptide #4.
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
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99US-00382950.
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Pred. No. 1.8e
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Pred. No. 1.8e+06;
1; Mismatches 0
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WPI; 2001-182803/18

Kurz M,

Lohse P,

Wagner

(PHYL-) PHYLOS INC.

19-JUL-2000; 2000WO-US019653.

99US-0145834P

01-FEB-2001. WO200107657-A1. Unidentified. Protein-RNA fusion; Strep-Tag II.

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Matches 6
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99US-00382950.
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Pred. No. 1.8e+06;
l; Mismatches 0;
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RESULT 5
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Best Local &
Matches
The present invention relates to a method of detecting mutations in a nucleic acid by amplifying the nucleic acid to produce a double-stranded amplicon, in vitro transcription and translation of this amplicon, and detection of the translated protein. The primers used for amplification are designed to produce an amplicon that is translatable and allows differentiation between translation products of wild-type and mutated nucleic acids. The method is used to detect mutations in tumour suppressor genes, for (early) diagnosis, monitoring and characterisation of tumours (especially of bladder and intestines) and in the germ line (using nucleic acids from embryos or blood cells). A new multi-tag vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a method for affixing a peptide acceptor to an RNA molecule through the formation of a covalent bond, noncovalent bond, or by chemical ligation. The method is useful for producing RNA-protein fusions which can be used for the isolation of proteins or nucleic aids with desired properties from large pools of partially or completely random amino acid or nucleic acid sequences. The present sequence is a Strep-Tag II used in the present invention
                                                                                                                                                                                                       Detecting mutations in nucleic acid, useful for diagnosis and characterization of tumors, by amplification, in vitro transc translation, then protein detection.
                                                                                                                                                                                                                                                                                                                     Kahmann S,
                                                                                                                                                                                                                                                                                                                                                                                  16-FEB-2001; 2001DE-01007317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutation detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Affixing a peptide acceptor to an RNA molecule useful for producing fusion proteins for isolating proteins or nucleic acids with desired properties through attachment of a peptide acceptor to the 3' end of
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                                                                                                                                                                          Fig 5; 62pp; German.
                                                                                                                                                                                                                                                                                                                     Mueller 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer; mutant; tag; tumour suppressor gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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85.7%;
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Pred. No.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GPCB-)
(MORP-)
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1.8e+06;
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antirheumatic, antiarthritic, neuroprotective, antiinflammatory, antidiabetic, antipsoriatic, immunosuppressive, dermatological, antithyroid, nephrotropic, thyromimetic and hepatotropic activit

activities,

and

for

The present invention describes a composition (1), comprising a polypeptide comprising an antibody-based antigen-hinding domain of human composition with binding specificity for an antigen expressed on the surface of a cell, where treating cells expressing the antigen with the polypeptides leads to suppression of an immune response, and the IC50 for the suppression of immune response is 1 microM or less. (1) has

Composition for suppressing immune response, treating diseases of immune system, has polypeptide comprising antibody-based antigen-binding domain of human composition, which binds antigen expressed on a cell surface.

Disclosure; Page 31;

139pp;

English

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RESULT 7
ABB77486
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Aba92469 to ABA92474 and ABB57457 to ABB7550 represent sequence used in
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                  The invention relates to a viral vector system for preparing recombinant adeno-associated virus (AAV) particles comprising, at least two plasmid vectors (ABL58983 and ABL58984) that include the two inverted terminal repeats (ITR) of AAV and additional sequences and plasmid vectors without ITRs but containing the rep and cap genes of AAV required for replication and packaging. The system is useful for producting recombinant AAV for production of a wide range of therapeutic glycoproteins in eukaryotic cells. The system provides efficient, large scale production of heterologous proteins in mammalian cells, without requiring an adenovirus heterologous proteins in mammalian cells, without requiring an adenovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vector system for preparing recombinant adeno-associated viral particles, used for high-level expression of heterologous therapeutic proteins in eukaryotic cells.
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                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 17; 59pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adeno-associated virus; AAV; glycoprotein; ITR; cap; rep; vector
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proteins in mammalian cells, without requiris not toxic to host cells and does not cause
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Pred. No. 1.8e+06;
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Best Local
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Best Local
                                                                                                     Matches
                                                                                                                                                                                                                                                                               This invention describes a novel method for the production of non-protein L-amino acids by the reaction of O-acetyl-L-serine with a nucleophile in the presence of a catalyst comprising O-acetyl-L-serine sulphydrylase at pH 5-7.4. The method of the invention is useful for the manufacture of pharmaceuticals and agrochemicals. In contrast to the process described in DE 10046934, a high nucleophile concentration can be used which includes toxic compounds. This sequence represents an affinity peptide containing a StrepTagII motif which is used in the construction of fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       produced proteins are highly pure. The present sequence is that of peptide tag, useful to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of non-protein L-amino acids useful for the manufacture pharmaceuticals and agrochemicals, comprises an enzyme catalyzed re of O-acetyl-L-serine with a nucleophile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2001;
03-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-protein L-amino acid; O-acetyl-L-serine; agrochemical production; nucleophile; O-acetyl-L-serine sulphydrylase; pharmaceutical producti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            StrepTagII affinity peptide
                                                                                                                                                                                                        Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maier T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2002; 2002EP-00007262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 8; 20pp; German.
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                                                                                                  6
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                                                                                                                              Similarity
SHPQFEK 8
                                                 XHPQFEK 8
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                                                                                                     Conservative
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2001DE-01021515.
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                                                                                                                              88.1%;
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Pred. No.
                                                                                                                              Score 37; DB 6;
Pred. No. 1.8e+06;
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                                                                                                        Mismatches
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for isolating mRNA from a population of cells. The method involves selectively isolating ribosomes or proteins that bind mRNA in a cell type specific manner and then isolating the mRNA bound to the ribosomes or proteins that bind mRNA. The method is useful for facilitating the analysis and quantification of gene expression in a selected cell type present within a heterogeneous cell mixture. The method may also be used in disgnostics or therapies for human diseases. The present sequence is Strep-tag II epitope peptide. This sequence is used to illustrate the method of the invention
21-MAR-2001; 2001DE-01013776.
                        02-OCT-2002
                                                 DE10113776-A1.
                                                                                                  Streptavidin;
                                                                                                                          Streptavidin 11 tag
                                                                                                                                                    28-MAR-2003
                                                                                                                                                                             ABP60361
                                                                                                                                                                                                                                                                                                                                                                   Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2, Page 121; 136pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolating cell-type specific mRNAs, useful in gene expression analysis quantification in a specific cell in a heterogeneous cell mixture, by isolating mRNA bound to ribosomes or proteins that bind mRNA in a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-430512/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-OCT-2001; 2001US-0340689P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene expression; therapy; isolation; epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strep-tag II epitope peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-AUG-2003
                                                                                                                                                                                                  ABP60361 standard; peptide; 8 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific manner.
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                                                                                                                                                                                                                                                                                          XHPQFEK 8
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                                                                                                                                                   (first entry)
                                                                                                 protein chip; microtitre plate; detection
                                                                                                                          peptide SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                             88.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shyjan AW,
                                                                                                                                                                                                                                                                                                                 Score 37; DB 6;
Pred. No. 1.8e+06;
1; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                         Length 8;
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RESULT 11
ABP60368
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Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at cleast one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, c.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-perative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin tag peptide disclosed with the invention
                                                                                                                                                                                                                                            DE10113776-A1.
                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                    Streptavidin;
                                                                                                                                                                                                                                                                                                                               Streptavidin binding peptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                             28-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                        ABP60368;
                                                                                                                                                                                                                                                                                                                                                                                                                   ABP60368 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 8; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-031166/03
                                                                                                Schmidt T;
                                                                                                                                                      21-MAR-2001; 2001DE-01013776.
                                                                                                                                                                                   21-MAR-2001; 2001DE-01013776
                                                                                                                                                                                                               02-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001DE-01013776
                                                                   WPI; 2003-031166/03.
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                                                                                                                           (BIOA-) INST BIOANALYTIK GMBH GOETTINGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XHPQFEK 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                    protein chip; microtitre plate; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
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85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37;
Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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protein, modules.

New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding

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RESULT 12
ADA09808
ID ADA09
XX ADA09
XX ADA09
XX ADA09
XX O6-NO
DT 06-NO
DE StepT
XX Non-r
KW cellu
KW dipyr
KW 4,4-d
KW human
XX 15-AU
PF 18-JU
XX 25-AU
PF 23-AU
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23-AUG-2000; 2000WO-US023233.
21-JUN-2002; 2002US-00049332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-JUN-2002;
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The present invention relates to non-radioactive markers used in the detection and analysis of nascent proteins translated in cellular or free translation systems. The preferred non-radioactive markers are

r or cell

use of a matrix concentrates the

interact low yields

Disclosure;

Page

15; 76pp; English

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RESULT 13
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      This invention describes a novel method of expressing genes in a cell-
free transcription and translation system which comprises using a
reaction solution containing all necessary components of the
transcription/translation system, amino acids, nucleotides and
metabolites that supply energy and that are needed for synthesis. The
proteins formed are immobilised on a matrix. The method allows simple
recovery of proteins without a separate isolation step and the amount o
proteins produced can be determined before a reaction is complete.
Continuous removal of proteins process, making possible synthesis of proteins that interact
expression process, making possible synthesis of proteins that interact
adversely with the process, so normally produced only in very low yield
the need of a matrix concess, so normally proteins that interact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dipyrrometheneboron difluoride (4,4-difluoro-4-bora-3a,4a-diaza-8-indacene) dyes. The detection method of the invention is a gel-free method that comprises introducing a modified nucleic acid template into a translation system under conditions such that a nascent protein is generated, the protein comprising at least an N-terminal marker. The method is useful in detecting, analysing and isolating nascent proteins produced in a cell-free or cellular translation system without the use of radioactive amino acids or other radioactive labels. Compositions comprising nascent proteins translated in the presence of markers may be used as vaccines or as drugs for humans and other animals. The method and a kit containing reagents for the detection of nascent proteins may be used as a rapid means to screen humans or other animals for the presence of certain diseases or disorders. The present sequence represents an epitope that can be used as an affinity marker for protein separation.
                                                                                                                                                                                                                                                 Claim 13; Col
                                                                                                                                                                                                                                                                                                    Expressing genes in cell-free system, useful for preparation of proteins, comprises that the protein formed is removed from solution by binding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell-free transcription system; protein synthesis; matrix; strep
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85.7%;
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Pred. No. 1.8e+06;
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This invention relates to novel truncated human aggrecanase proteins and nucleotide sequences. Aggrecan is a major extracellular component of articular cartilage. It is a proteoglycan responsible for providing cartilage with its mechanical properties of compressibility and elasticity. The loss of aggrecan has been implicated in the degredation of articular cartilage in arthritic disease implicated in the degredation of articular cartilage in arthritic disease such as osteoarthritis. Aggrecanase is responsible for the cleavage of aggrecan, thereby having role in cartilage degradation associated with osteoarthritis and inflammatory joint disease. The proteins of the current invention are truncated aggrecanase-1 (ADAMTS-4) and aggrecanase-2 (ADAMTS-5) enzymes which have at least one thrombospondin (TSP) domain deleted. These are biologically active and have greater stability and higher expression that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to proteins of any size. This sequence represents a highly conserved peptide from E. coli streptavidin which is used to illustrate the med of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New biologically-active aggrecanase protein having a deletion
a portion of a TSP domain, useful for treating osteoarthritis,
Parkinson's disease, coronary thrombosis, Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aggrecanase; aggrecan; articular cartilage; proteoglycan; cartilage compressibility; cartilage elasticity; arthritic disease; osteoarthritis; cartilage degradation; inflammatory joint disease; osteoarthritis; cartilage degradation; inflammatory joint disease; aggrecanase-1; ADAMTS-4; aggrecanase-2; ADAMTS-5; thrombospondin domain; TSP domain; osteopathic; antiarthritic; cytostatic; antiinflammatory; antirheumatic; ophthalmological; thrombolytic; vasotropic; antimicrobial; respiratory-gen; nootropic; neuroprotective; antiparkinsonian; immunosuppressive; aggrecanase inhibition; cancer; rheumatoid arthritis; septic arthritis; corneal ulceration; coronary thrombosis; Crohn's disease; emphysema; Alzheimer's disease; parkinson's disease; multiple activation; carcer; release; carting the coronary disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 18; 111pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multiple sclerosis.
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Matches
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                                                                           The invention comprises a drug composition consisting of hollow nanoparticles which enclose a drug substance and which present a specific antibody on their surface. The drug composition is usef cell or tissue specific treatment of cancer and virus infections present amino acid sequence was used in the exemplification of t
                                                                                                                                                                                                                                                                                                                            Hollow protein nanoparticles enclosing a c
tissue or cell specific antibody at their
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21-FEB-2003; 2003JP-00045088.
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US10B_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US10B_PUB.pep:*

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19: /cgn2_6/ptodata/2/pubpaa/US10B_PUB.pep:*
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                      Length
  US-09-809-517A-9
US-09-973-145-7
US-09-813-197-8
3 US-10-104-218-5
3 US-10-208-357-9
4 US-10-026-578B-2
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4 US-10-026-578B-7
4 US-10-264-127-8
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Sequence 11, Appl
Sequence 7, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 9, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 7, Appli
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### ALIGNMENTS

US-10-026-578B-11

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; FEATURE:
, NAME/KEY: misc_feature
, OTHER INFORWATION: Artificial Sequence represents
US-10-026-578B-11
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: 1BA (GmbH)
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICATION Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta FILLE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT APPLICATION NUMBER: DE 10 11 3 776.1
PRIOR APPLICATION NUMBER: DE 10 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PRILING DATE: 2001-01-12
SUCTURARE: PATENTIAN DATE: 2001-03-13
SSEQ ID NO 11
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/10026578B Publication No. US20030083474A1 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                                               FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9). (28)
OTHER INFORMATION: Of the five (GGGS) repeats between position 9 and 28, one or more OTHER INFORMATION: repeats may be missing. However, at least one (GGGS) repeat will OTHER INFORMATION: be present
                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
90.5%;
75.0%;
Score 38; Pred. No.
  DB 14;
11;
                         Length 36
                                                                                                       peptide binding module
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CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
VUMBER OF SEQ ID NOS: 41
SOFTWARE: Patehtin version 3.0
SEQ ID NO 9
                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/973,145
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/382,950
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US Patent No. US20020132248A1
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Patent No. US20020034733A1
GENERAL INFORMATION:
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OTHER INFORMATION: Synthetic
-09-973-145-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Olbjnik, Jerzy
TITLE OF INVENTION: N-Terminal and C-Terminal Markers
FILE REPERENCE: AMBER-06819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rothschild, Kenneth J. APPLICANT: Gite, Sadanand APPLICANT: Olejnik, Jerzy
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
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85.7%;
                                                                                              88.1%;
                                                  Score 37; DB 9; Le
Pred. No. 1.2e+06;
1; Mismatches 0;
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Pred. No. 1.2e+06;
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RESULT 6
US-10-208-357-9
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; NAME/KEY: PEPTIDE
; LOCATION: (1)..(8)
; OTHER INFORMATION: StrepTagII affinity peptide for protein
US-10-104-218-5
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US-10-104-218-5
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Publication No. US20020177196A1
GENERAL INFORMATION:
APPLICANT: MAIER, Thomas
APPLICANT: GAEBERT, Carsten
                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GAEBERT, CARSten
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PROTEINOGENIC L-AMINO ACIDS
FILE REPERENCE: MAIER, T. ET AL. -2
CURRENT APPLICATION NUMBER: US/10/104,218
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: German No. US20020177196A1 101 16 881.0
PRIOR PILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/09813197 Publication No. US20050009013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Rothschild, Kenneth
APPLICANT: Gite, Sadanand
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Prot
FILE REFERENCE: AMBER-03951
CURRENT FILLING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 18
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
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                                                                                                                                   Score 37; DB 13;
Pred. No. 1.2e+06;
1; Mismatches 0
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Pred. No. 1
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1.2e+06;
                                                                                                                                                                      Length 8;
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; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: designed sequence to act as an identifying tag
US-10-208-357-9
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TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR APPLICATION NUMBER: 60/145,834
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                     RESULT 8
US-10-026-5788-2
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SEQ ID NO 8

LENGTH: 8

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: STREP tag
                                                                                       Sequence 2, Application US/10026578B Publication No. US20030083474A1 GENERAL INFORMATION:
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Matches 6; Conserv
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Publication No. US20020182687A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/001,934
CURRENT FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 63
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TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING
TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR
FILE REFERENCE: GPCG-P01-003
APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kurz, Markus
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6; Conserva
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85.7%;
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Pred. No. 1.2e+06;
1; Mismatches 0
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RESULT 10 US-10-174-368A-7

Sequence 7, Application US/10174368A Publication No. US20030092031A1 GENERAL INFORMATION:
APPLICANT: Rothschild, Kenneth J. APPLICANT: Gite, Sadanand APPLICANT: Olejnik, Jerzy

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                                                                                                                                                              ; NAME/KEY: misc feature ; OTHER INFORMATION: Artificial Sequence represents peptide binding module US-10-026-578B-9
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LENGTH: 8
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application US/10026578B
Publication No. US20030083474A1
GENERAL INFORMATION:
APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
                                                                                               Query Match
Best Local Similarity
                                                                              Matches
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                                                                                                                                                                                                                                   FEATURE: OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                   LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
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OTHER INFORMATION: Art
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OTHER INFORMATION: Synthetic Peptide
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                                                                                                 88.1%;
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85.7%;
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Pred. No. 1.2e+06;
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Pred. No. 1.2e+06;
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CURRENT APPLICATION NUMBER: US/10/174,368A
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/049,332
PRIOR APPLICATION NUMBER: PCT/US00/23233
PRIOR APPLICATION NUMBER: PCT/US00/23233
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 1909-08-25
PRIOR APPLICATION NUMBER: 09/382,736
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
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US-10-264-127-8
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; OTHER INFORMATION: Synthetic
US-10-264-127-8
                                                                                                          US-10-339-712-8
                                                                                                                        RESULT 12
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Publication No. US20030190643A1
GENERAL INFORMATION:
APPLICANT: Rothschild, Kenneth
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Protection Reference: AMBER-03951
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Best Local S
Matches 6
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CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: US/09/382,736B
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
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Best Local
Sequence 8, Application US/10339712
Publication No. US20040014071A1
GENERAL INFORMATION:
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
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les 6; Conserv
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nilarity 85.7%;
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Pred. No.
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PRIOR APPLICATION NUMBER: 10/049,322
PRIOR APPLICATION NUMBER: 10/049,322
PRIOR EILING DATE: 2002-06-21
PRIOR EILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/382,736
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
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US-10-339-712-67
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CURRENT FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: 10/049,322
PRIOR PILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: PCT/US00/23233
PRIOR APPLICATION NUMBER: PCT/US00/23233
PRIOR PILING DATE: 2000-08-23
PRIOR PILING DATE: 1990-08-25
PRIOR PILING DATE: 1999-08-25
PRIOR PILING DATE: 1999-08-25
PRIOR PILING DATE: 1999-08-25
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Best Local Similarity 85..
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SEQ ID NO 67
LENGTH: 8
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TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent
TITLE OF INVENTION: Proteins
FILE REFERENCE: AMBER-07199
CURRENT APPLICATION NUMBER: US/10/339,712
CURRENT FILING DATE: 2003-01-10
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Best Local Similarity
Matches 6; Conser
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APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
APPLICANT: Lim, Mark
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 1.2e+06;
1; Mismatches
                                                                                                                                                                       Score 37; DB 15;
Pred. No. 1.2e+06;
1; Mismatches 0
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RESULT 14 US-10-275-046-4

; Sequence 4, Application US/10275046

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RESULT 15
US-10-425-000-76;
US-10-425-000-76;
Sequence 76, Application US/10425000
Publication No; US20040052777A1
GENERAL INFORMATION:
APPLICANT: Nedbit, Mark
APPLICANT: Nedbit, Mark
APPLICANT: Blanche, Francis
TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
TITLE OF INVENTION: Angiogenesis
FILE REFERENCE: ST01027-B
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: US/10/425,000
CURRENT FILING DATE: 2003-04-29
PRIOR APPLICATION NUMBER: 10/233,675
PRIOR FILING DATE: 2002-09-04
NUMBER OF SEQ:ID NOS: 105
SOFTWARE: Patentin version 3.2
SEQ:ID NO 76
LEUGTH: 8
TYPE: PRT
ORGANISM: Ardificial Sequence
PEATURE:
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POTHER INFORMATION: Purification tag
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TITLE OF INVENTION: IMMUNOMODULATORY HUMAN MHC CLASS II ANTIGEN-BINDING POLYPEPTIDES
FILE REFERENCE: GPCG-P01-260
CURRENT APPLICATION NUMBER: US/10/275,046
CURRENT FILING DATE: 2002-10-31
PRIOR FILING DATE: 2002-10-31
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NUMBER: 00110063.5
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 8
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Search completed: March Job time : 24.878 secs
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Best Local Similarity 85.7%;
Matches 6; Conservative
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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### SUMMARIES

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Sequence 48074, A	e e	e 3797,	æ	e 4700	е 7	e 71,	, 9	e 12;	Sequence 11, Appl	e 10,	е 9,	е 8	e 7,	2	e 4.	e 34	e 31,	e 33	e 30,	e 6,	e 9,	S	e 9,	Sequence 8, Appli	e 7,		rip

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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	aprianhae
4868, Ap	11, Appl	32254, A	42719, A	2, Appli	27, Appl	12, Appl	6, Appli	6, Appli	6, Appli	6, Appli	6, Appli	6, Appli	43549, A	18407, A	48154, A	32937, A	3071/, M

# ALIGNMENTS

WS-09-382-950-7  i Sequence 7, Application US/09382950  patent No. 6303337  i GENERAL INFORMATION:  APPLICANT: Rothschild, Kenneth  APPLICANT: Gite, Sadanand  APPLICANT: Olejnik, Jerzy  i TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Prot  FILE REFERENCE: AMBER-03879  CURRENT APPLICATION NUMBER: US/09/382,950  CURRENT FILING DATE: 1999-08-25  NUMBER OF SEQ ID NOS: 17  SOFTWARE: Patentin version 3.0  SEQ ID NO 7  LENGTH: 8  TYPB: PRT  ORGANISM: Artificial/Unknown	Query Match  88.1%; Score 37; DB 3; Length 8;  Best Local Similarity 85.7%; Pred. No. 4.1e+05;  Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps  Qy 2 XHPQFEK 8  :       Db 2 SHPQFEK 8	-2 Application US/08948097C 6103493 ORWATION: Skerra, Arne Voss, Selma WNENTION: Streptavidin Muteins ENCE: HUBR 1119 PLICATION NUMBER: US/08/948,097C LING DATE: 1997-10-09 PLICATION NUMBER: DE 196 41 876.3 LING DATE: 1996-10-10 SEQ ID NOS: 17 Artificial sequence BINDING ORWATION: Binding ligand for streptavid-

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US-09-613
Sequence 9, Appilication (Sequence 9), Appilication (Sequence 9), Appilication (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequence 9), Appilicant (Sequen
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; LOCATION: ()...()
; OTHER INFORMATION: Synthetic
US-09-382-950-7
                   Query Match
Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rothschild, Kenneth
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Prot
FILE REFERENCE: AMBER-03951
CURRENT APPLICATION NUMBER: US/09/382,736B
CURRENT FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 8
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Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                        OTHER INFORMATION: designed sequence to act as an identifying
                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
PEATURE:
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             Score 37; DB 4;
Pred. No. 4.1e+05;
1; Mismatches 0
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Pred. No. 4.1e+05;
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; LOCATION: (1)..(8)
; OTHER INFORMATION: StrepTagII affinity peptide for protein purification
US-10-104-218-5
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Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on FILE REFERENCE: MORPHO/11
CURRENT FILING DATE: 2001-03-15
CURRENT TILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 90103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PAtentin version 3.0
TENERAL BEST PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PATENT NUMBER: PAT
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Matches 6; Conserv
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APPLICANT: MAIER, Thomas
APPLICANT: GAEBERT, Carsten
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PROTEINOGENIC L-AMINO ACIDS
FILE REFERENCE: MAIER, T. ET AL. -2
CURRENT APPLICATION NUMBER: US/10/104,218
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: German No. 6579705 101 16 881.0
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-05-03
NUMBER OF SED ID NOS: 5
PRIOR FILING DATE: 2001-05-03
NUMBER OF SED ID NOS: 5
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Patent No. 6579705
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TYPE: PRT
ORGANISM: artificial sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
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2 XHPQFEK 8 : | | | | | | |
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                                                                                               Score 37; DB 4; Length 8; Pred. No. 4.1e+05; Indels 1; Mismatches 0; Indels
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Pred. No. 4.1e+05;
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RESULT 9
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US-09-809-517A-6
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APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins of the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention in the coring of invention of invention in the coring of invention of invention in the coring of invention of invention in the coring of invention of invention in the coring of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of invention of inventinvention of invention of invention of invention of invention of i
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APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILLING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 90103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
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Best Local Similarity
Matches 6; Conserv
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Patent No. 6753136
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Best Local Similarity
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TYPE: PRT
ORGANISM: artificial sequence
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TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 31
LENGTH: 24
TYPE: PRT
ORGANISM: artificial sequence
FEATURE: PRT
ORGANISM: Artificial sequence
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                                                                                                            RESULT 11
US-09-809-517A-34
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APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
TITLE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILMS DATE: 2001-03-15
CURRENT FILMS DATE: 2001-03-15
Sequence 34, Application US/I
Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 675:
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Best Local Similarity
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Pred. No. 1.1;
1; Mismatches
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Pred. No.
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6753136el methods for displaying (poly)peptides/proteins on

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GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
IIILE OF INVENTION: Metal Binding Proteins, Rec
IIITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION UNMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
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US-09-809-517A-34
                                                                                                                                                                                 Sequence 5, Application US/09977137A
Patent No. 6750042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PACENTIN Ver. 2.0
SEQ ID NO 4
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0 SEQ ID NO 34 LENGTH: 25
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APPLICANT: Cagulat, Jonathan
TITLE OP INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: particles via disulfide bonds FILE REFERENCE: MORPHO/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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Pred. No.
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                                                                                                  Recombinant Host
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; OTHER INFORMATION: Description of Artificial Sequence:
US-09-977-137A-5
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                                                   NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                   Sequence 8, Application US/09977137A Patent No. 6750042 GENERAL INFORMATION:
                                                                                                  TITLE OF INVENTION: Metal Binding Proteins, TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
TITLE OF INVENTION: MUBBER: US/09/977,137A
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEC IN NOC. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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SEQ ID NO 7
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 5
LENGTH: 117
TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                   APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
                                   ENGTH: 117
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Pred. No. 6.3;
1; Mismatches
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Pred. No. 6.3;
1; Mismatches
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6.3;
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Page 5
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Search completed: March 2, 2005, 12:25:35 Job time : 10.1057 secs	Qy 2 XHPQFEK 8 :      Db 111 SHPQFEK 117	Query Match 88.1%; Score 37; DB 4; Length 117; Best Local Similarity 85.7%; Pred. No. 6.3; Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	, FEATURE: , OTHER INFORMATION: Description of Artificial Sequence: chelon US-09-977-137A-8

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Copyright
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: March 2, 2005, 12:20:44; Search time 6.11382 Seconds (without alignments)
 125.901 Million cell updates/sec

Title: Perfect score: Scoring table: Sequence: 1 rxhpqfer 8

BLOSUM62DX Gapop 10.0 , 283416 seqs, 96216763 residues Gapext 0.5

Searched:

283416

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*

₫.,

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

# SUMMARIES

29	28	27						21				17	16	15						y		7		ហ		w		<b>-</b>	:	No. Score	Result
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78.6	•	•	78.6	•	•	٠		81.0		81.0	۲	81.0	81.0	81.0	81.0	81.0	۲	81.0	•	۲	81.0	•	ω.	83.3	83.3	œ	88.1	92.9		Match	Query
452	360	347	332	310	105	3791	3746	918	845	755	627	621	543	808	376	360	355	313	213	189	142	55	420	338	129	362	300	360		Length	
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F84421	F83203	885640	AF3304	C84701	T00283	YGPLV8	YGPLV3	A55277	T07052	H72262	T00484	A71516	A84134	C82138	C75580	T18140	T24938	H69297	AD2533	T36642	B82223	T35092	871199	T30538	A82547	H75131	G75436	B71073		ID	
hypothetical prote	probable ATP-bindi	hypothetical prote	m	pr	hypothetical prote	alpha-aminoadipyl-	alpha-aminoadipyl-	hexokinase (EC 2.7	probable potassium	sensor histidine k	hypothetical prote		acetolactate synth	conserved hypothet	μ.		hypothetical prote		•		hypothetical prote	probable small hyd		heat shock protein	hypothetical prote	malate dehydrogena	conserved hypothet	probable malate de		Description	

### ALIGNMENTS

# B71073 probable malate dehydrogenase - Pyrococcus horikoshii C;Species: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 12-Jul-2004 C;Accession: B71073

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: B71073 R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-360 <KAW>

A;Cross-references: UNIPROT:059028; GB:AP000005; NID:g3236132; PIDN:BAA30380.1; PID:g325 A;Experimental source: strain OT3 A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

Best Loc Matches Query Match Local Similarity 6; Conserv Conservative 92.9%; Score 39; Pred. No. 2; Mismatc ed. No. 6.4; Mismatches DB 2; 0; Length 360; Indels 0 Gaps 0;

A;Gene: PH1277

Genetics:

밁 S 311 RKHPEFER 318 1 RXHPOFER 8

conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004

C;Accession: G75436
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999 J.D.; Dodson, R.J. T.; Zalewski, C.;

A; Title: Genome sequence of A; Reference number: A75250; the radioresistant bacterium Deinococcus radiodurans MUID:20036896; PMID:10567266

R1

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A; Reference number: A; Accession: G75436

A; Status: preliminary

A;Molecule type: DNA A;Residues: 1-300 <WHI> A;Residues: 1-300 <WHI> A;Cross-references: UNIPROT:Q9RVC9; GB:AE001960; GB:AE000513; NID:g6458833; PIDN:AAF1067 A;Experimental source: strain R1 C;Genetics: A;Gene: DR1100

A;Map position: 1 C;Superfamily: Escherichia coli yceA protein

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A; Cross references: UNITROT: OSPAKO; GB: AE004059; GB: AE003849; NID: G9107718; PIDN: AAP8531 A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asriones, M.R.S.; Bueno, M.R.D.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajian, J.P.; Krieger, J.E.; Kuramae, B.E.; Laiguchado, M.A.; Madeira, M.M.E.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.A.; H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
                                 A;Reference number: A59328
A;Contents: annotation
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A82547
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nature 406, 151-157, 2000
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 bel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein XF2515 [imported] - Xylella fastidiosa (strain 9a5c) C;Species: Xylella fastidiosa (c;Caces: Xylella fastidiosa C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: A85247
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome seque
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A; Residues: 1-129 <SIM>
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999
C;Accession: H75131
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A;Experimental source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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A; Accession: H75131
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probable small hydrophilic protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35092
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Accession: Tab

Harris, D.; Bentley,

S.D.; Parkhill, J.; Barrell, B.G.; Rajandream,

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A; Gene: dnaJ
C; Superfamily:
F; 4-70/Domain:
RESULT 7
                                                                                                            Query Match
Best Local Similarity
Whitehes 5; Conserve
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C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology F;14-75/Domain: dnaJ amino-terminal homology <DNJ>
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A,Accession: 871199
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A;Residues: 1-420 <ZHO>
A;Cross-references: UNIPROT:Q42530; EMBL:U22340; NID:g1872162; PIDN:AAB49030.1; PID:g727
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S71199
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A;Title: Conserved organization of genes in trypanosomatids. A;Reference number: Z16580; MUID:98418771; PWID:9747975
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C;Species: Trypanosoma cruzi
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C;Genetics:
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Pred. No. 35;
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thaliana homologue
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RXHPQFE

Page 3

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A;Cross-references: UNIPROT:Q9S2S6; EMBL;AL096884; PIDN:CAB51455.1; GSPDB;GN00070; A;Experimental source: strain A3(2) C;Genetics:
                                                                                                                                                                                                                              R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, June 1999
A;Reference number: 221610
A;Accession: T36642
                                                                                                                                                                                                                                                                                                              hypothetical protein SCH35.17 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 00-Dec_1999 #sequence_revision 03-Dec_1999 #text_change 09-Jul-2004 C;Accession: T36642
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein VC1253 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Species: Vibrio cholerae C;Datc: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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                                                                                                                             A;Cross-references: UNIPROT:Q9X8Y9; EMBL:AL078610; PIDN:CAB44410.1; A;Experimental source: strain A3(2)
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A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-142 <HEI>
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A; Residues: 1-55 < SEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, July 1999
A;Reference number: Z21567
                                                                                                                           A; Experimental source: strain
                                                                                                                                                                    A; Residues: 1-189 <OLI>
                                                                                                                                                                                       A; Molecule type: DNA
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les 5; Conserv
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62.5%;
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75.0%;
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Pred. No. 22;
2; Mismatches
                     Score 34;
Pred. No.
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Pred. No. 7
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RESULT 11
H69297
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C;Accession: AD2533
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, & R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, & R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, T.; Sasamoto, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;Kaneko, & R;
                                                                                       hypothetical protein T15H9.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tC;Accession: T24938
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R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.B.; Ketchum, K.A.; Dodson; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Wenth, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Wenth, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Wenth, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Wenth, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Reference number: A69250; MUID: 98049343; PMID: 9389475
A;Accession: H69297
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1-213 <KUR>
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A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AD2533
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AD2533
hypothetical protein alr7551 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120br hypothetical protein alr7551 [imported] - Nostoc sp. (strain PCC 7120 C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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    R;Gardner, A. submitted to the EMBL
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                                                                                                                                                                                                                                                                                                                    RESULT 12
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A;Experimental source: strain PCC 7120
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A;Residues: 1-313 <KLE>
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5; Conserve
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; Yasuda, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not
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C;Accession: C75580

R;White, O.; Bisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A73250; MUID:20036896; PMID:10567266

A;Accession: C75580
                                                                                                                                                                                                                                                                                                                                              adenine deaminase-related protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec_1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
C75580
                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 <WHI>
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T18140
                                                                 A;Cross-references: UNIPROT:Q9RYP2; GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF123
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:O41120; EMBL:U42580; NID:g4028896; PIDN:AAC96965.1
A;Experimental source: specific host Chlorella strain NC64A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Graves, M.V.; Van Etten, J.L. submitted to the EMBL Data Library, May 1999 A;Reference number: Z18806 A;Recession: T18140
                                                               A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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A;Introns: 42/3; 74/3; 129/3; 151/3; 208/3; 249/2; 290/3
C;Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
F;24-89/Domain: dnaJ amino-terminal homology <DNJ>
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A;Accession: T74030
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A;Residues: 1-360 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein A638R - Chlorella virus PBCV-1
C/$Decies: Chlorella virus PBCV-1
C/$Dete: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: CESP:T15H9.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Molecule type: DNA
;Molecule type: DNA
;Residues: 1-355 <WIL>
;Cross-references: UNIPROT:Q10005; EMBL:Z47356; PIDN:CAA87414.1; GSPDB:GN00020; CESP:T1
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Best Local
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Best Local Similarity
Matches 5; Conserv
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position: 2
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5; Conserv
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62.5%;
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71.4%;
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Pred. No. 59;
2; Mismatches
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Pred. No. 58;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                 E.K.; Peterson, J.D.; Dodson, L.; Utterback, T.; Zalewski,
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C.; Ma
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RESULT 15
C82138
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C; Superfamily: hypothetical protein b1706
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Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera patho A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: March Job time: 7.11382 secs
                                                                                                                                                                                                                                               A;Gene: VC1931
                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9KQR7; GB:AE004269; GB:AE003852; NID:g9656466; PIDN:AAF9507
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein VC1931 [imported] - Vibrio cholerae (strain N16961 serogr C;Species: Vibrio cholerae
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Best Local S
Matches 5
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Best Local
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                                                                                              2 XHPQFER
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5; Conservative
                                                                                                                                         Conservative
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              'n
                                                                                                                                                                                                                                                                                                                                                                                      both chromosomes of the cholera pathogen Vibrio cholerae.
35; MUID:20406833; PMID:10952301
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                2005, 12:28:55
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Pred. No. 85;
                                                                                                                                         Mismatches
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H.; Dragoi, I.; Sellers, P
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No.
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Maximum Match 100%
Listing first 45 summaries
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31098
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seq length: 2000000000
       Match
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137.824 Million cell updates/sec
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1: uniprot_sprot:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Q7y820
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9 bradyrhizob
7 lactobacill
                                                                                                                                      6 streptomyce
2 drosophila
4 abies alba
3 vibrio chol
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prunus aviu
bordetella
bordetella
  streptomyce
bartonella
drosophila
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deinococcus
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RESULT 2  MDH PYRHO  ID MDH PYRHO  STANDARD; PRT; 360 AA.  AC 059028;  DT 30-MAY-2000 (Rel. 39, Created)  DT 30-MAY-2000 (Rel. 39, Last sequence update)  DT 30-MAY-2000 (Rel. 39, Last annotation update)  DT Malate dehydrogenase (EC 1.1.1.37).  GN Name=mdh; OrderecLocusNames=PH1277;  OS Pyrococcus horikoshii.  OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;  OX NCBI_TaxID=53953;  RN [1]	Query Match 92.9%; Score 39; DB 2; Length 313; Best Local Similarity 75.0%; Pred. No. 20; Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps Qy 1 RXHPQFER 8  :  :   Db 182 RHHPQYER 189	ISUBS-Testis;  ISUBS-Testis;  ISUBS-Testis;  Paci O., Sahin U., Koslowski M., Buss B., Bell C., Ball cc, C., Schir U., Koslowski M., Buss B., Bell C., Ball cck C., Eberle T., Zuber M., Villena-Heinsen C., Seitz eundschuh M.;  novel tumour associated leucine zipper protein targeti gene transcription and splicing.";  gene transcription and splicing.";  ogene 21:3879-3888 (2002).  DUENCE FROM N.A.  son S.;  son S.;  son S.;  son S.;  son S.;  son S.;  son S.;  Li, AF124430; AAF28870.1;  Li, AF124430; AAF28870.1;  LI, AF124430; AAF28870.1;  DUENCE 313 AA; 35937 MW; E041911D9BA1DC8B CRC64;  DUENCE 313 AA; 35937 MW; E041911D9BA1DC8B CRC64;	RESULT 1  Q9P127  Q9P127;  AC Q9P127;  DT 01-OCT-2000 (TrEMBLrel. 15, Created) DT 01-CT-2000 (TrEMBLrel. 27, Last sequence update) DT 01-Strubles antigen (DJ237H22.1).  BE HOM-TES-85 tumor antigen (DJ237H22.1).  GN Name=dJ237H22.1;  OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  RP SEQUENCE FROM N.A.	32 34 81.0 213 2 Q8ZSF9 33 34 81.0 240 2 Q6TBT6 34 81.0 313 1 Y384 ARCFU 35 34 81.0 315 2 Q7VL01 35 34 81.0 335 2 Q7VL01 36 34 81.0 342 2 Q8TKF9 37 34 81.0 342 2 Q8TKF9 38 34 81.0 342 2 Q8TKF9 39 34 81.0 342 2 Q8TKP9 39 34 81.0 359 2 Q41120 39 34 81.0 366 2 Q9W083 40 34 81.0 366 2 Q9W083 41 34 81.0 366 2 Q9W083 42 34 81.0 386 2 Q9FUP2 41 34 81.0 386 2 Q9FUP2 41 34 81.0 386 2 Q9FUP2 42 34 81.0 386 2 Q9FUP2 43 34 81.0 386 2 Q9SUP3 44 34 81.0 396 2 Q726V6 45 34 81.0 402 Q83AS1 46 34 81.0 418 2 Q9M554 47 34 81.0 418 2 Q9M554 48 34 81.0 418 2 Q9M554 49 34 81.0 439 1 IDG1_DROYA ALIGNMENTS
va e e e e e e e e e e e e e e e e e e e	Gaps 0;	į	ni.	anabaena sp uncultured archaeoglob prochloroco methanosarc oryza sativ paramecium drosophila deinococcus metarhizium desulfovibr coxiella bu euphorbia e drosophila

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RESULT 3
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Best Local Similarity
Matches 6; Conserv
                                      radiodurans R1.",
Science 286:1571-1577(1999).
-!- SIMILARITY: Belongs to the UPF0176 family
-!- SIMILARITY: Contains 1 rhodanese domain.
                                                                                                          SEQUENCE FROM N.A.

STRAIN-R1 / ATCC 13939 / DSM 20539 / NCIB 9279;

MEDLINE-20036896, PubMed=10567266; DOI=10.1126/Science.286.5444.1571;

White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,

Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,

Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,

Vamathevan J.J., Lam P., McDonald L.A., Utterback T.R., Zalewski C.,

Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,

Ketchum K.A., Nelson K.E., Salzberg S.L., Smith H.O., Venter J.C.,

"Fraser C.M.,"
                                                                                                                                                                                                                                                                                                                                    Q9RVC9;
28-FEB-2003
28-FEB-2003
25-OCT-2004
                                                                                           "Genome sequence of the radioresistant bacterium
                                                                                                                                                                                                                                                                  Deinococcus radiodurans.
Bacteria; Deinococcus-Thermus;
Deinococcaceae; Deinococcus.
                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
25-CCT-2004 (Rel. 45, Last annotation update)
Hypothetical UPF0176 protein DR1100.
                                                                                                                                                                                                                                                                                                         OrderedLocusNames=DR1100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@eisb-sib.ch).
                                                                                                                                                                                                                                                        NCBI_TaxID=1299;
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Pfam; PF0261b; Ldh 2; 1.

Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid SEQUENCE 360 AA; 39751 MW; 6E9D8B16ECDE6E6F CRC64;
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SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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Pred. No. 24;
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shii OT3.";
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Horikoshi K.,
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RESULT 4
MDH P
ADD MDH P
AC Q9VOD
DT 16-OC
DT 16-OC
DT 16-OC
DT Malatt
GN Name=
CO Pyroo
OX Pyroo
OX Pyroo
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W MEDLINE-GES / Orsay;

W ACOhen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte V., Potent G.N., Forterre P.;

WA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,

Wan der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;

"An integrated analysis of the genome of the hyperthermophilic RT archaeon Pyrococcus abyssi.";

Whol. Microbiol. 47:1495-1512(2003).

CC -!- CATIVITY: (S) malate + NAD(+) = oxaloacetate + NADH.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCILIULAR LOCATION: Cytoplasmic (Probable).

CC -!- SIMILARITY: Belongs to the LDH2/MDH2 oxidoreductase family.
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Best Local
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PIR; G75436; G75436.
TIGR; DR1100; -.
HAMAP; MF 00469; -; 1.
InterPro; IPR001792; Acylphosphatase.
InterPro; IPR001763; Rhodanese-like.
Pfam; PF00581; Rhodanese; 1.
                                                    Pfam; PF02615; Ldh 2; 1.

Complete proteome; NAD; Oxidoreductase; Tricarboxylic acid
SEQUENCE 362 AA; 39907 MW; 1E15C2E9E6BA5012 CRC64;
                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDH PYRAB
Q9V0D5;
16-OCT-2001
                                                                                                                                                                                             EMBL; AJ248285; CAB49769.1; -. PIR; H75131; H75131.
                                                                                                                                                            InterPro; IPR003767; ldh_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=GE5 / Orgay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UU-2004 (Rel. 44, Last annotation update)
Malate dehydrogenase (EC 1.11.37)
Name=mdh; OrderedLocusNames=PYRABO8550; ORFNames=PAB1791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pyrococcus abyssi.
Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=29292;
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SMART; SM00450; RHOD; 1
PROSITE; PS50206; RHODAN
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75.0%;
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"A pollen-expressed gene for a novel protein wit

fis very tightly linked to a gene for S-RNase in

Prunus cerasus and P. avium.";

Plant Cell Physiol. 44:764-769(2003).

EMBL; AB096857; BAC681148.1; -.

InterPro; IPR0006527; F-box.

InterPro; IPR0006527; F-box assoc 1.

InterPro; IPR0006527; F-box assoc 1.

InterPro; IPR000504; RNA_rec_mot.

Pfam; PF00646; F-box; 1.

SMART; SM00256; FBOX; 1.

SMART; SM00256; FBOX; 1.

SMART; SM00256; FBOX; 1.

SMART; SM00256; FBOX; 1.

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STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

MEDILINE-22827954; PubMede-12910771; DOI=10.1038/ng1227;

Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R., Mungall K.L.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,

Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Feltwell T., Goble A., Norberczak H., O'Neil S., Ormond D., Price C.,
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01-OCT-2003 (TrEMBLrel. :
01-MAR-2004 (TrEMBLrel. :
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01-OCT-2003 (TrEMBLrel. 2:
Hypothetical protein.
OrderedLocusNames-BP0636;
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Bacteria, Proteobacteria,
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01-OCT-2003
01-OCT-2003
                                        Q8XRVO PRELIMINARY; PRT; 557 AA.

Q8XRVO;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PROBABLE TREHALOSE-6-PHOSPHATE SYNTHASE (ALPHA, ALPHA-TREHALOSE-PHOSPHATE SYNTHASE UDP-FORMING) PROTEIN (EC 2.4.1.15).
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SETRAINARB50 / ATCC BAA-588;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;

Mungall K.L.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,

Chilling-orth T., Collins M., Cronin A., Davis P., Doggett J.,

Chilling-worth T., Collins M., Cronin A., Davis P., Doggett J.,

Chilling-worth T., Collins M., Cronin A., Davis P., Doggett J.,

Chilling-worth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;

Comparative analysis of the genome scene of Rorderella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete
SEQUENCE
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EMBL; BX640412; CAE44962.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Comparative analysis of the Bordetella parapertussis and Nat. Genet. 35:32-40(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella bronchiseptica (
Bacteria; Proteobacteria; E
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
OrderedLocusNames=BB4712;
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                               Name=RS01697; OrderedLocusNames=RSp0731
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                                                                                                                                                                                                                                     Polyprotein.
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HSSP; Q88590; 1TMF.
G0; G0:0019028; C:viral capsid; IEA.
G0; G0:0005198; F:structural molecule
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STRAIN-5-D-VII;

MEDLINE=21105197; PubMed=11160660;

DOI=10.1128/JVI.75.4.1620-1631.2001;

Zell R., Dauber M., Krumbholz A., Henke A., Birch-Hirschfeld E.,

Stelzner A., Prager D., Wurm R.;

"Porcine teachoviruses comprise at least eleven distinct serotype molecular and evolutionary aspects.";

J. Virol. 75:1620-1631(2001).
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EMBL, AL646080; CAD17882.1; -.
EMBL, AL646080; CAD17882.1; -.
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Burkholderiaceae;
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Bacteria, Proteobacteria,
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larity 75.0%;
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Pred. No. 1.9e+02;
1; Mismatches 1
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                                     01-UUN-2003 (TrEMBLrel. 24, C
01-UUN-2003 (TrEMBLrel. 24, I
01-UUN-2003 (TrEMBLrel. 24, I
Conserved domain protein.
OrderedLocusNames=CBU1308;
                                                                                                                    Q83C26;
Bacteria; Proteobacteria;
Coxiellaceae; Coxiella.
                             Coxiella burnetii.
                                                                                                                                                                                                                                                                                                                          SEQUENCE 129 AA;
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EMBL, AE004059, ARBS313.1; -.
PIR, A82547; A82547.
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Q9PAK0;
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OrderedLocusNames=Xf2515;
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         Gammaproteobacteria; Legionellales;
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                                               EMBL; AE016822; AAT90014.1; -.

GO; GO:0051082; F:unfolded protein binding; IEA.

GO; GO:0006457; P:protein folding; IEA.

GO; GO:0006457; P:protein folding; IEA.

InterPro; IPR002939; DnaJ C.

InterPro; IPR001623; DnaJ N.

InterPro; IPR001623; DnaJ N.

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InterPro; IPR0018971; HSP40 DnaJ pep.

InterPro; IPR0018971; HSP DnaJ Pefam; PF00226; DnaJ; 1.

Pfam; PF00226; DnaJ; 1.

PFAM; PR00625; DNAJ C; 1.

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PROSITE; PS00636; DNAJ 1; 1.

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25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
25-OCT-2004 (TrEMBLrel. 2
DnaJ proteid.
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Kitajima J.P., Truffi D., do Amaral A.M., Harakava R.,
de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
Almeida N.F. Jr., Carrer H., Coutinho L.L., El-Dorry H.A.,
Ferro M.I.T., Gagllardi P.R., Giglioti E., Goldman M.H.S.,
Goldman G.H., Kimura B.T., Ferro E.S., Kuramae E.E., Lemos B.G.M.,
Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,
Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,
Taai S.M., Zanca A.S., Simpson A.J.G., Brumbley S.M., Setubal J.C.;
"The genome Bequence of the Gram-positive sugarcane pathogen Leifsonia
xyli subsp. xyli.";
Mol. Plant Microbe Interact. 17:827-836 (2004).
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EMBL; AE016964; AA090814.1; -.
TIGR; CBU1308; -.
Complete
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MEDLINE-22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E.,
Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
"Complete genome sequence of the Q-fever pathogen, Coxiella"
                             Chaperone;
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Leifsonia xyli (subsp. xyli).
Leifsonia xyli (subsp. xyli).
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InterPro; IPR002939; DnaJ_C.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR001623; DnaJ_N.
InterPro; IPR003095; Hsp_DnaJ_pep.
InterPro; IPR003095; Hsp_DnaJ.
Pfam; PF00226; DnaJ; 1.
Pfam; PF00226; DnaJ; 1.
PRINTS; PR00625; DNaJ; 1.
PRINTS; PR00625; DNAJPROTEIN.
SMART; SM00271; DnaJ; 1.
PROSITE; PS00636; DNAJ_1; 1.
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Eukaryota; Euglenozoa;
EUKaryota; Euglenozoa;
NCBI_TaxID=5693;
"A DnaJ-like protein
                                                                                                                                                                                  Co-chaperone protein.
Name=DnaJ-like;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=DNAJ;
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MEDLINE=21570179; PubMed=11551903; DOI=10.1074/jbc.M102427200 Salmon D., Montero-Lomeli M., Goldenberg S.; "A DnaJ-like protein homologous to the yeast co-chaperone Sis
                                                                     SEQUENCE FROM N.A.
                                                                                                           Eukaryota; Euglenozoa;
NCBI_TaxID=5693;
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GO; GO:0006457; P:protein folding; IEA.
InterPro; IPR00239; DnaJ CXXCXGXG.
InterPro; IPR001305; DnaJ CXXCXGXG.
InterPro; IPR001305; DnaJ N.
InterPro; IPR001623; DnaJ N.
InterPro; IPR003095; Hsp-DnaJ pep.
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PROSITE; PS00637; DNAJ 1; 1.
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PROSITE; PS0076; DNAJ 2; 1.
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J. Biol. Chem. 276:43970-43379 (2001).

EMBL; AF345336; AAK19734.1; -.

HSSP; P25685; IHDJ.

GO; GO:0051082; F:unfolded protein binding; IE;
GO; GO:006457; P:protein folding; IEA.

InterPro; IPR00123; DnaJ_C.

InterPro; IPR00123; DnaJ_N.

InterPro; IPR003095; HSP40 DnaJ_pep.

InterPro; IPR003095; HSP40 DnaJ_pep.
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 26,
Q1-MAR-2004 (TrEMBLrel. 26,
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"AtJ3 (Accession No. U22340), an Arabidopsis thaliana J-Protein Homologous to Saccharomyces cerevisiae YDJ1p. (PGR99-162).";
Plant Physiol. 121:1053-1054 (1999).
EMBL; U22340; AAB49030.1; -.
PIR; S71199; S71199.
HSSP; P25665; 1HDJ.
                                                                                                                    Chaperone;
SEQUENCE
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MEDLINE=20027448; PubMed=10557255;
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pfam; pF01556; DnaJ C; 1.
prints; pR00625; DNAJPROTEIN.
smart; SM00271; DnaJ; 1.
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GenCore version (c) 1993 - 2005

5.1.6 Compugen Ltd.

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### SUMMARIES

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### ALIGNMENTS

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28-MAR-2002; 2002EP-00007401

05-NOV-2001; 2001JP-00379298. 25-JAN-2002; 2002US-00350978.

(HELI-) HELIX RES INST

(REAS-) RES ASSOC BIOTECHNOLOGY.

Isogai T, Sugiyama T, Yamamoto J, Isono Y, Seki N, Yoshikawa T, Otsuki T, Wakamatsu A, Sato H, I, Hio Y, Otsuka K, Nagai K, Irie R, Otsuka M, Nagahari K, Masuho Y; Ishii S; Tamechika ı,

WPI; 2003-450961/43. N-PSDB; ADB63452.

New polynucleotides and polypeptides, useful for developing a diagnostic marker or medicines for regulation of their expression and activity, or as targets of gene therapy.

Claim 1; Page; 222pp; English.

The invention discloses a polynucleotide comprising a sequence selected from 1970 fully defined nucleotide sequences which encode novel polypeptides. Also claimed is a polypeptide encoded by the polynucleotide or its partial peptide, an antibody binding to the polypeptide or peptide of the polynucleotide, immunologically assaying the polypeptide or peptide peptide of the polynucleotide by contacting the polypeptide or peptide

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Matches 6
                 The present invention describes a method for diagnosing a disorder characterised by expression of a human cancer associated antigen (CAA) precursor (I) coded by a NA Group 1 nucleic acid molecule (N1) comprising contacting the biological sample with an agent (A) that specifically binds to N1, (I) or its fragment, complexed with an human leukocyte
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties.

Claim 1; SEQ ID NO 20354; 122pp; English.

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                                                                                                                                                 New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                                                               (HINK/)
(SLAT/)
(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; pathogen tolerance; pest tolerance; plant growth regulator; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; himologous recombination; seed oil yield; protein yield; carbohydrate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and N1 or (I). (I) has cytostatic activity and can be used in gene therapy and vaccine production. The method can be used for treating a subject with a condition characterised by expression of (I) in cells c subject. ARB75607 and ARB75608 represent proteins from human cancer associated antigen precursors, and ARB75609 to ARB75802 represent HLA class I binding motifs in human cancer associated antigen precursors given in the exemplification of the present invention
                                                                                                                                                                                                                             Cao Y,
                                                                                                                                                                                                                                                                                                                         21-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                 20-FEB-2003; 2003US-00369493
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                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria
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CHEN X.
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polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic formar from the printed specification but was obtained in electronic
 The invention relates to a recombinant DNA promoter functional in a plant cell, where provide for expression of a polynucleotide
                                                                                                New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                            Cao Y,
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(SLAT/)
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                                                                     Claim 1;
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                                                                                                                                                                                                                                        ) CAO'Y.
) HINKLE G J.
) SLATER S C.
) CHEN X.
) GOLDMAN B S.
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75.0%;
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construct comprising a the promoter is positioned a encoding a polypeptide from
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                                                                                                                              Skerra
                                                                                                                                                                                                                                                           25-MAY-1994.
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heavy chain v
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                                                                                                                                                                                                                                                                                                                            terminus
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terminus of VH chain"
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Disclosure; Page 11;

53pp; English

New fusion peptide(s) - have easily capable of binding to streptavidin.

have easily

controlled binding properties

and

are

N-PSDB; AAQ62669. WPI; 1994-153484/19.

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                                                Six derivatives of pASK46 (a plasmid for expression of the D1.3Fv fragment in E.coll) were produced which encode 4 different peptides at the C-terminus of VH and 2 peptides at the C-terminus of VL of the D1.3Fv fragment. The peptides fused to the C-terminus are all examples of streptavidin-binding peptides corresponding to a generic formula (see AAR52698). The peptides do not interfere with the protein function but facilitate purification by conferring streptavidin-binding properties on the fusion protein
                                                                                                                                                                                                                                                                                                   Disclosure; Page 11; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1994-153484/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skerra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide tag.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pASK46-pllXH encoded C-terminal streptavidin-binding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR52693;
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                                                                                                                                                                                                                                                                                                                                                            fusion
able of
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binding to
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variable
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terminus of VH chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; fusion protein; immunog:
affinity chromatography;
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Sequence

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ADS43180

standard; protein;

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                                                                                    Six derivatives of pASK46 (a plasmid for expression of the D1.3Fv fragment in E.coli) were produced which encode 4 different peptides the C-terminus of VI of the fragment. The peptides fragment. The peptides fused to the C-terminus are all examples of streptavidin-binding peptides corresponding to a generic formula (s AAR52698). The peptides do not interfere with the protein function facilitate purification by conferring streptavidin-binding properti
                                                                          AAR52698). The peptides facilitate purification the fusion protein
                                                          Sequence
                                                                                                                                                                 Disclosure; Page 11; 53pp; English.
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                                                                                                                                                                                                                                             Skerra A,
                                                                                                                                                                                                                                                                                 03-NOV-1992;
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terminus of VL chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein;
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    have easily
streptavidin.

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                     Mismatches
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3.7;
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CC transformed plant having an improved property. The plant is a crop plant CC transformed plant having an improved property comprises transformed plant with the CC having an improved property comprises transformed plant with the CC recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the CC improved plant properties e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of protein yield and/or CC phosphorus use and/or uptake, by modification of protosynthesis or by condition, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan CC production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
Sequence 362 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 21610; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-FEB-2003; 2003US-00369493.
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SLATER S C.
CHEN X.
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                                       at segdata.uspto.gov/sequence.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen
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                                                                                                    recombinant vector comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The nucleic acids are chosen from 3654 disclosed sequences encoding 3654 disclosed proteins. The nucleic acids is useful for diagnosing pathological conditions resulting from E. faecium bacterial infection (e.g. urinary tract infection, bacteraemia, endocarditis, wounds and abdominal-pelvic infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida albicans derived peptides or antisense polypeptides. Pharmaceutical compositions and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents one if the disclosed E. faecium proteins.
                                                                        Sequence 482 AA;
                                                                                                                                                                                                                                                                                                                                         Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 sequential nucleotides chosen from any of the nucleic acids, its complement or sequences hybridising to it). Also included and a complement or sequences hybridising to it). Also included and the complement of sequences hybridising to it).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 4868; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide useful for detection, prevention and treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ADC91587.
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14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid derived from
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98US-0085598P.
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                                                                                  cc the 5213 antisence sequences given in the specification where expression cc of the nucleic acid inhibits proliferation of a cell. Also included are: cf (1) a vector comprising a promoter operably linked to the nucleic acid (2) a vector comprising a promoter operably linked to the nucleic acid (2) a host cell containing the vector; (3) an isolated cc nucleic acid; (4) an antibody capable of specifically binding cp polypeptide; (5) producing the polypeptide; (6) producing the polypeptide; (6) producing the polypeptide; (6) producing the polypeptide; (6) inhibiting cellular cc proliferation or the activity of a gene in an operon required for proliferation, or that has an activity against a biological pathway compound that influences the activity of identifying a gene required for cellular proliferation or the biological pathway of required for proliferation, or that inhibits cellular proliferation; (8) cc required for proliferation, or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a cc organism acts; (9) manufacturing an antibiotic; (10) profiling a cc organism acts; (9) manufacturing an antibiotic; (10) profiling a cc pathway in which a proliferation of the trains; or (13) identifying the target of a compound that inhibits proliferation of compound that inhibits proliferation of the strains is present in a culture or collection of compound that inhibits the compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits the compound that inhibits are useful for compound that inhibits are useful for compound that inhibits are useful 
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25-CCT-2001; 2001US-0342923P
08-FEB-2002; 2002US-00072851
06-MAR-2002; 2002US-0362699P
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Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 47374; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins a antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-FEB-2002; 2002WO-IB002069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New protein from Neisseria gonorrheae, useful for the manufacture medicament for treating or preventing N. gonorrheae infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 708; 815pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 418 AA;
                                                                                                                                                                     ABB62997 standard; protein; 749 AA
                       Drosophila melanogaster polypeptide SEQ ID NO 15783
                                                                         26-MAR-2002
                                                                                                                        ABB62997;
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Pred. No. 4.3e+02;
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Pred. No. 4.3e+02;
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Best Local Similarity
Matches 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016140-ABL16175) and the encoded protteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                        Streptomyces hygroscopicus
                                                                                                                                                                                         Streptomyces hygroscopicus non-ribosomal peptide synthetase
                                                                                                                                                                                                                      29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                   29-MAR-2002; 2002US-0368713P
                                                             28-MAR-2003; 2003WO-US009746
                                                                                       09-OCT-2003
                                                                                                                WO2003082909-A1
                                                                                                                                                                 Peptide synthetase; enzyme; antibiotic; mppA; AC98
                                                                                                                                                                                                                                                                         ADE86071 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 15783; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001; 2001WO-US009231
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                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                         protein; 2747 AA
                                                                                                                                                                                                                                                                                                                                                                                                        83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , DWG
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                                                                                                                                                                                                                                                                                                                                                                                                        8.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conjugates a serine to a glycine to produce a peptide. The peptide is then conjugated (through the glycine) to a phenylalanine. Each amino acid is incorporated into the peptide chain by a unique module. After addition of the phenylalanine, the peptide chain is then transferred to the mppB component. MppA is about 295 kba. The invention provides a method of producing NRPS using transformed host cells. It also provides a method of producing a cyclic peptide antibiotic, such as AC98, using the NRPS comprised of mppA and mppB. The antibiotic is preferably a lipoglycopeptide antibiotic with activity against Gram-positive pathogens. Also provided are methods of modifying NRPS, e.g. by replacement of an adenylation domain, to produce an antibiotic having a modified peptide core, and a method for evaluating the structural regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2747 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replacement of an adenylation domain, modified peptide core, and a method for the modified peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               components, mppA and mppB ADE86072, both involved in the synthesis of core AC98. MppA is composed of 3 minimal modules, where each module i comprised of an adenylation, thiolation and condensation domain. MppA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is the protein sequence of mppA, a component of non-ribosomal peptide synthetase (NRPS) from Streptomyces hygroscopic NS17 (NRRL 30439) that is responsible for the production of cyclic peptide antibiotic AC98. The NRPS complex exists as 2 separate
                              WPI; 1998-218868/20
                                                            Skerra A,
                                                                                                                                                                  09-OCT-1997;
                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                        Streptavidin; ligand; binding affinity; mutant; isolation; purification;
                                                                                                                                                                                                                                                                                                                                                         Streptavidin tagged peptide ligand #2.
                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                              AAW59212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New non-ribosomal peptide synthetase, useful for preparing antibacterial peptides, derived from Streptomyces, also related nucleic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hucul JA, Macgarvey N,
                                                                                                                                                                                                    15-APR-1998
                                                                                                                                                                                                                                    EP835934-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW59212 standard;
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                                                                                                (BIOA-) INST BIOANALYTIK GMBH
                                                                                                                                10-OCT-1996;
                                                                                                                                                                                                                                                                                                     recover; immobilise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                Voss
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                                                                                                                                  96DE-01041876.
                                                                                                                                                                  97EP-00117504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Greenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthesis of the
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Streptavidin mutants with higher binding affinity for peptide ligands

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Query Match
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                                                The present invention describes a method of detecting nascent proteins involving aminoacylating a tRNA molecule with a 4,4-difluoro-4-bora-3A,4A involving aminoacylating a tRNA molecule with a 4,6-difluoro-4-bora-3A,4A diaza-s-indacene (BODIPY) marker leading to the production of a misaminoacylated tRNA. This enables the detection, isolation and analysis of nascent proteins using UV without the usual accompanying radioactivity problems. It may be used to detect mutations, for example in cancer, Duchenne muscular dystrophy, adenomatous polyposis coli and colon cancer
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                                                                                                                                                                                                                                                                                                                                     Method for detecting nascent proteins by fluorescence comprises misaminoacylating a tRNA molecule with a marker compound, useful for detecting mutations in proteins, e.g. cancer.
Sequence 8 AA;
                                                                                                                                                                                                                                                                                     Disclosure; Page 47; 204pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-168972/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rothschild KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-1999;
25-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nascent protein detection; protein analysis; aminoacylated tRNA; BODIFY market; disease diagnosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMBE-) AMBERGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity les 5; Conserv
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99US-00382950.
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Pred. No.
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Query Match
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps

Qy 2 XHPQFER 8
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Db 2 SHPQFEK 8
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Search completed: March 2, 2005, 13:02:46
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Result
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                              Score
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1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

3: /cgn2=6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

4: /cgn2=6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

5: /cgn2=6/ptodata/2/pubpaa/US07 NEW PUB.pep:*

6: /cgn2=6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

7: /cgn2=6/ptodata/2/pubpaa/US08 NEW PUB.pep:*

9: /cgn2=6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

9: /cgn2=6/ptodata/2/pubpaa/US08 PUBCOMB.pep:*

10: /cgn2=6/ptodata/2/pubpaa/US09 PUBCOMB.pep:*

11: /cgn2=6/ptodata/2/pubpaa/US09E PUBCOMB.pep:*

12: /cgn2=6/ptodata/2/pubpaa/US09C PUBCOMB.pep:*

13: /cgn2=6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

14: /cgn2=6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

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16: /cgn2=6/ptodata/2/pubpaa/US10B PUBCOMB.pep:*

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     GenCore version 5.1.6
Copyright (c) 1993 - 2005: Compugen Ltd.
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15 US-10-369-493-20354
15 US-10-369-493-1288
15 US-10-369-493-21610
15 US-10-282-122A-47374
14 US-10-282-122A-47374
15 US-10-026-578B-11
15 US-10-026-578B-1
16 US-10-102-842-2
17 US-10-102-145-7
18 US-10-104-218-5
18 US-10-104-218-5
19 US-10-104-218-5
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19 US-10-208-357-9
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Sequence 11, Appl
Sequence 2, Appli
Sequence 9, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 8, Appli
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                                                                                                                                                                                                   Sequence 3576, Ap
Sequence 20354, A
Sequence 1288, Ap
Sequence 21610, A
Sequence 47374, A
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ALIGNMENTS

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9,	e 8,	7,	5,	е4,	e 10,	34,	е 4,	e 3,	31,	33,	30,	30	25	29	e 20,	Sequence 6, Appli	u L	8, 7	e 11	e 17,	e 41,	e 23,	e 25,	e 76,	е4,	e 67,	Sequence 8, Appli	ев,	e 7,	e 9,	е 2

# RESULT 1 US-10-104-047-3576 US-10-104-047-3576 ; Sequence 3576, Application US/10104047 ; Publication No. US20030236392A1 ; Publication No. US20030236392A1e1 ; APPLICANT: HELIX RESEARCH INSTITUTE ; TITLE OF INVENTION: No. US20030236392A1e1 full length cDNA ; FILE REFERENCE: H1-A0.05 ; CURRENT APPLICATION NUMBER: US/10/104,047 ; CURRENT FILING DATE: ; PRIOR APPLICATION NUMBER: US/10/104,047 ; CURRENT FILING DATE: ; NUMBER OF SEQ ID NOS: 4096 ; SOFTWARE: Patentin Ver. 2.1 ; SOFTWARE: Patentin Ver. 2.1 ; SOFTWARE: Patentin Ver. 2.1 ; SOFTWARE: Homo sapiens US-10-104-047-3576 Query Match Best Local Similarity 75.0%; Pred. No. 50; Matches 6; Conservative 2; Mismatches 0; Gaps ON 1 RXHPOFER 8 | | | | | | | | | Db 100 RHHPOYER 107

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RESULT 2 US-10-369-493-20354

Sequence 20354, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.

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Best Local Similarity
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US-10-369-493-1288
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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US-10-369-493-20354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10 (52052) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR FILING DATE: 2002-02-21 NUMBER OF SEQ ID NOS: 47374.

SEQ ID NO 1288 LENGTH: 360
                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                         Sequence 21610, Application US/10369493 Publication No. US20030233675A1
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 20354
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APPLICANT:
APPLICANT:
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Best Local Similarity 75.0%;
                                                                                                APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
                   APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXCRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
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APPLICANT: Chen, Xianieng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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Pred. No.
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; ORGANISM: Burkholderia cepacia US-10-282-122A-47374
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                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILLING DATE: 2000-09-09
PRIOR FILLING DATE: 2000-10-23
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: 2000-10-23
PRIOR PRIOR PRIOR DATE: 2000-11-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILLING DATE: 2000-11-22
PRIOR PRIOR PRIOR NUMBER: 60/257,931
Query Match
Best Local Similarity 75.0
Conservative
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Best Local S
Matches 6
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LENGTH: 362
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/267,636 PRIOR FILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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tes 6; Conserv
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Yamamoto, Robert
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Malone, Cheryl
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                              Score 36; DB 15; Length 619; Pred. No. 4.4e+02; 1; Mismatches 1; Indels
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Pred. No. 1.7e+02;
1; Mismatches 1
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; TYPE: PRT
; ORGANISM: Streptomyces hygroscopicus
US-10-402-842-2
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10402842 Publication No. US20030219872A1 GENERAL INFORMATION:
                                                                                                                                                        SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 2747
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                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                APPLICANT: Magarvey, Nathan A.
APPLICANT: Hucul, John A.
APPLICANT: Hucul, John A.
TITLE OF INVENTION: NOW. RIBOSOMAL PEPTIDE SYNTHETASES AND ASSOCIATED BIOSYNTHETIC GEN
FILE REFERENCE: 0630/1J854-US1
CURRENT APPLICATION NUMBER: US/10/402,842
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: US 60/368,713
PRIOR FILING DATE: 2002-03-30
PRIOR FILING DATE: 2002-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity '
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: midc_feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (9). (28)
OTHER INFORMATION: Of the five (GGGS) repeats between position 9 and 28, one or more OTHER INFORMATION: repeats may be missing. However, at least one (GGGS) repeat will OTHER INFORMATION: be present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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5; Conserv
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                       Conservative
                                    83.3%;
75.0%;
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                   Score 35; DB 15;
pred. No. 2.8e+03;
1; Mismatches 1
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                                                       DB 15; Length 2747;
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                     Indels
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RESULT 8
US-09-809-517A-9
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                                                                                                                                                US-09-973-145-7
                                                                                                                                                                                                                                                                                         APPLICANT: Rothschild, Kenneth J.
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
FILE REFERENCE: AMBER-06819
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US/09/973,145
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/882,950
PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOUTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 8
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Best Local Similarity
Matches 5; Conserv
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LENGTH: 8
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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Best Local Similarity
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Patent No. US20020132248A1
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CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NO. US20020034733A1el methods for displaying (poly)peptides/proteTITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lohning,
                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: Synthetic
                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                TYPE: PRT
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SHPQFEK 8
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71.4%;
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Pred. No. 1.2e
2; Mismatches
                                                                                    Score 34; DB 9;
Pred. No. 1.2e+06
                                                                         Mismatches
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1.2e+06;
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US-10-208-357-9
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 ; Sequence 9,
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Best Local Similarity
""" hes 5; Conserva
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; OTHER INFORMATION: Synthetic US-09-813-197-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: MAIER, Thomas
APPLICANT: GAEBERT, Carsten
APPLICANT: GAEBERT, Carsten
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PROTEINOGENIC L-AMINO ACIDS
FILE REFERENCE: MAIER, T. ET AL.-2
FILE REFERENCE: MAIER, T. ET AL.-2
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US/10/104,218
CURRENT FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
                                                                                                                                                                                                    Query Match
Best Local &
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Publication No. US20050009013A1
GENERAL INFORMATION:
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APPLICANT: Gite, Sadanand
APPLICANT: Gite, Sadanand
APPLICANT: Oligink, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Prot
FILE REFERENCE: AMBER-03951
CURRENT APPLICATION NUMBER: US/09/813,197
CURRENT FILING DATE: 2001-03-20
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: German No. PRIOR FILING DATE: 2001-05-03 NUMBER OF SEQ ID NOS: 5
                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(0)
OTHER INFORMATION: StrepTagII affinity peptide for protein
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                              2 XHPQFER 8
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5; Conserv
Application US/10208357
No. US20020182687A1
                                                                                                             SHPOFEK 8
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Pred. No.
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1.2e+06;
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US-10-026-578B-2
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US-10-001-934-8
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APPLICANT: Lohse, Peter
APPLICANT: Hose, Peter
APPLICANT: Magner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR FILING DATE: 2000-07-19
PRIOR FILING DATE: 1990-07-27
NUMBER OF SEQ ID NOS: 26
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US-10-001-934-8
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Sequence 2, Application US/10026578B
Publication No. US20030083474Al
GENERAL INFORMATION:
APPLICANT: IEA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/10001934

Publication No. US20030032782A1

GENERAL INFORMATION:
APPLICANT: NAGY, ZOLTAN

TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
FILE REFERENCE: GPCG-P01-003

CURRENT APPLICATION NUMBER: US/10/001,934

CURRENT FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 63

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 8
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Best Local Similarity 71.4
Matches 5; Conservative
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FEATURE:
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TYPE: PRT
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Pred. No. 1.2e+06;
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Pred. No. 1.2e+06;
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PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 8
TYPE: PRT
ORGANISM: artificial sequence
Search completed: March Job time: 24.878 secs
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; OTHER INFORMATION: Synthetic Peptide
; FEATURE;
; NAME/KEY: misc feature
; OTHER INFORMATION: Artificial Sequence represents peptide binding module
US-10-026-578B-2
                                                                                                                                                                                                                                                              US-10-026-578B-9
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US-10-026-578B-9
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                                                                                                                                  Query Match
Best Local Similarity 71.-
Thes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IBÁ (GmbH)
APPLICANT: IBÁ (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
CURRENT PRILICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-10-12
NUMBER: PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTMARE: PACENTIN Version 3.1
SEQ ID NO 9
LENGTH: 8
TYPE: PRI
ATTIFICIAL SCREENS
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/10026578B Publication No. US20030083474A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Synthetic Peptide
                                                                              2 XHPQFER 8 :|||||: 2 SHPQFEK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SHPQFEK 8
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                                                                                                                                                                    81.0%; Score 34; DB 14; Length 8; 71.4%; Pred. No. 1.2e+06; ative 2; Mismatches 0; Indels
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
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seq length: 2000000000
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Match Length DB
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1: /cgn2_6/ptcdata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptcdata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptcdata/1/1aa/6B_COMB.pep:*
6: /cgn2_6/ptcdata/1/1aa/backfIles1.pep:*
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Sequence 4868, Ap

Sequence 32326, A

Sequence 27, Appli

Sequence 7, Appli

Sequence 8, Appli

Sequence 9, Appli

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Sequence 30, Appli

Sequence 30, Appli

Sequence 31, Appli

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US-09-107-532A-4868

RESULT 1

ALIGNMENTS

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Sequence 5521, Ap	Sequence 16778, A	Sequence 13, Appl	Sequence 13, Appl	Sequence 24, Appl	Sequence 4, Appli	Sequence 17, Appl	Sequence 17, Appl	Sequence 2, Appli	Sequence 11, Appl	Sequence 17585, A	Sequence 25397, A	Sequence 42719, A	Seguence 41422, A	Sequence 2, Appli	Sequence 27, Appl	Sequence 12, Appl	Sequence 43549, A

### NAME/KEY: misc\_feature LOCATION: (B) LOCATION 1...482 SEQUENCE DESCRIPTION: SEQ ID NO: 4868: US-09-107-532A-4868 Sequence 4868, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION: TELEFAX: (781)893-8277 INFORMATION FOR SEQ ID NO: 4868: SEQUENCE CHARACTERISTICS: CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-un-1998 PRIOR APPLICATION NUMBER: 60/085,598 PRIOR APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 FILING DATE: 1017 FILING DATE: 1017 FILING DATE: 1017 FILING DATE: 1017 ATTORNEY/AGENT INFORMATION: NAME: Ariniello, Pamela Deneke REGISTRATION NUMBER: 40,489 REFERENCE/DOCKET NUMBER: GTC-012 TELECOMMUNICATION INFORMATION: TELEPHONE: (781)893-5007 LENGTH: 482 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE: COMPUTER READABLE FORM: MEDIUM TYPE: CD/ROM ISO9660 COMPUTER: PC APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACID ENTEROCOCCUS FEATURE: CORRESPONDENCE ADDRESS: ADDRESSEE: GENOME THERAPEUTICS CORPORATION NUMBER OF SEQUENCES: STREET: 100 B COMPUTER: PC OPERATING SYSTEM: <Unknown> ORGANISM: Enterococcus faecium ZIP: 02354 STATE: Massachusetts COUNTRY: USA 100 Beaver Street 7310 and David Bush AND AMINO ACID SEQUENCES RELATING TO FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

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GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 128
TYPE: PRT
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Best Local S
Matches 5
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 47543
LENGTH: 128
TYPE: PRT
      Sequence 2, Application US/08948097C
Patent No. 6103493
GENERAL INFORMATION:
APPLICANT: Skerra, Arne
APPLICANT: Voss, Selma
TITLE OF INVENTION: Streptavidin Muteins
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Best Local
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FILE REFERENCE:
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tes 6; Conserv
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Pred. No.
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US-09-382-736B-8
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APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: W-Terminal and C-Termi
FILE REFERENCE: AMBER-03879
CURRENT APPLICATION NUMBER: US/09/382,950
CURRENT FILING DATE: 199-08-25
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-382-950-7
                                                                  Sequence 8, Application US/09382736B
Patent No. 6306628
GENERAL INFORMATION:
APPLICANT: Rothschild, Kenneth
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Prot
FILE REFERENCE: AMBER-03951
CURRENT APPLICATION NUMBER: US/09/382,736B
CURRENT FILING DATE: 1999-08-25
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SEQ ID NO 2
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8
LENGTH: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Best Local
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OTHER INFORMATION: Binding ligand for streptavidin
3-08-948-097-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/08/948,097C CURRENT FILING DATE: 1997-10-09 EARLIER APPLICATION NUMBER: DE 196 41 876.3 EARLIER FILING DATE: 1996-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Rothschild, APPLICANT: Gite, Sadana APPLICANT: Olejnik, Jei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial/Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic
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                                                                                                                                                                                                                                                                                                                  SHPQFEK
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Pred. No.
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Pred. No.
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4.1e+05;
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GENERAL INFORMATION:

APPLICANT: Kúrz, Markus

APPLICANT: Kúrz, Markus

APPLICANT: Wagner, Richard

ITITLE OF INVENTION: Peptide Acceptor Ligation Methods

FILE REFERENCE: 50036/031002

FULRENT APPLICATION NUMBER: US/09/619,103

CURRENT APPLICATION NUMBER: 05/145,834

PRIOR APPLICATION NUMBER: 260/145,834

PRIOR APPLICATION NUMBER: 26
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)...(8)
; OTHER INFORMATION: StrepTagII affinity peptide for protein purification
US-10-104-218-5
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
US-10-104-218-5
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US-09-619-103-9
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Best Local Similarity 71.
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Patent No. 6579705
GENERAL INFORMATION:
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Best Local Similarity
Matches 5; 'Conserv
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SEQ ID NO 9
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ORGANISM: Artificial Sequence
PEATURE:
PEATURE:
OTHER INFORMATION: designed sequence to act as an identifying
-09-619-103-9
                                                                                                                                                            APPLICANT: MAIE, Thomas
APPLICANT: MAIE, Thomas
APPLICANT: GABBERT, Carsten
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PROTEINOGENIC L-AMINO ACIDS
FILE REFERENCE: MAIER, T. ET AL.-2
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: GERMAN NO. 6579705 101 16 881.0
PRIOR FILING DATE: 2001-04-04
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: German NO. 6579705 101 21 515.0
PRIOR PILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
                                                                                           ORGANISM: Artificial
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71.4%;
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71.4%;
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Pred. No.
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TYPE: PRT
; TYPE: PRT
; PRANISM: artificial sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-9
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US-09-809-517A-9
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Best Local Similarity
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                                                                                                                                  APPLICATION: No. 6753136el methods for displaying (poly)peptides/proteins on TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 10
TYPE: PRT
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Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
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Best Local
Query Match 81.0%; Score 34; DB 4; Length 10; Best Local Similarity 71.4%; Pred. No. 1.5; Matches 5; Conservative 2; Mismatches 0; Indels
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                                                                                                OTHER INFORMATION: Description of Artificial Sequence: synthetic module
                                                                                                                    ORGANISM: artificial sequence FEATURE:
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5; Conserv
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71.4%;
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Pred. No. 4.1e+05;
2; Mismatches C
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Pred. No. 4.1e
2; Mismatches
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US-08-687-559-30
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Patent No. 5955647
                                                                                                                                                                                                    Sequence 30, Application US/09401415 Patent No. 6503732
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APPLICANT: Fitchen, John H.
APPLICANT: Beachy, Roger N.
APPLICANT: Beachy, Roger N.
TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS
TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
                                                                                              Itent No. 6503734
Itent No. 6503734
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
REPUBLICANT: THE SCRIPPS RESEARCH INSTITUTE
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
OVERPRODUCE PEPTIDES AND PROTEINS
OVERPRODUCE PEPTIDES AND PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-678-5099 (NFORMATION FOR SEQ ID NO: 30:
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OPERATING SYSTEM: Windows95
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: 07302/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424

RIOR APPLICATION DATA:

REPLICATION NUMBER: PCT/U895/01467

FILING DATE: 03-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
mes 5; Conserv
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                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensle
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                                                                                                                                                                                                                                                                                                                        GHPÖFOR 13
                CITY: Los Angeles
STATE: California
                                                    ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Fish & Richardson, P.C. 4225 Executive Square, Suite 1400
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COUNTRY: USA
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5955647ember 18, 1996
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US-09-809-517A-30
                                                                        , OTHER INFORMATION; Description of Artificial Sequence: synthetic module us-og-809-517a-30
                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
ITTLE OF INVENTION: No. 6753136el methods for displaying (poly) peptides/proteins on
ITTLE OF INVENTION: particles via disulfide bonds
ITTLE OF INVENTION: particles via disulfide bonds
ITTLE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION UNMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOCTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 21
TYDE: DBT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/09809517A Patent No. 6753136
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Matches
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                              TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bostich, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: FD-4074
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
5; Conserve
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/01467 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-Sep-1999 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
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  Conservative
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                    71.4%;
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Score 34; DB 4; pred. No. 3.4; 2; Mismatches
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Sequence 31, Application US/09809517A
Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lokining, Corinna
ITILE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b
ITILE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b
ITILE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b
ITILE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b
ITILE OF INVENTION: NO. 6753136el methods for displaying (poly)peptides/proteins on b
ITILE OF INVENTION: NUMBER: US/09/809,517A
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR PILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 31
LENGTH: 24
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
FEATURE:
FEATURE:
FORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-31
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US-09-809-517A-33
Search completed: March Job time : 9.10569 secs
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US-09-809-517A-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: NO. 6753136el methods for displaying (poly) peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
                                                                                                                                                                      Query Match 81.0%; Score 34; DB 4; Length 24; Best Local Similarity 71.4%; Pred. No. 4; Matches 5; Conservative 2; Mismatches 0; Indels
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Best Local Similarity 71.4%;
Matches 5; Conservative
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Patent No. 6753136
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                    2, 2005, 12:25:35
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; Pred. No. 3.6;
2; Mismatches
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Page 5

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No.
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Perfect score:
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seq
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length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
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124
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6
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd
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A54281
A44063
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S60712
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T173627
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AH2925
F98356
F98356
RGBYC5
C48560
F90197
D41732
JQ2183
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A90904
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4.5	44	43	42	41	40	39	38	37	36	35	34	ယ ယ	32	31	30
43	43	43	43	43	43	43	43	43.5	43.5	43.5	44	44	44	44	44
34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	35.1	35.1	35.1	35.5	35.5	35.5	35.5	35.5
251	234	216	209	187	172	68	55	597	597	597	1253	507	365	342	330
N	N	N	N	ν	N	N	N	N	N	_	N	μ	N	N	N
C81816	D96592	G75128	C89005	A45878	D82642	E85918	I78887	A90770	E85632	HQECL	T21065	QQBE41	AD1634	S37596	AC2071
- F	hypothetical prote	hypothetical prote	protein T24A6.3 [i	hypothetical prote	conserved hypothet	hypothetical prote	hypothetical Nf-1	hydrogenase-1 larg	hydrogenase-1 larg	hydrogenase (EC 1.	hypothetical prote	BGLF1 protein - hu	X-Pro dipeptidase	protein kinase MCP	hypothetical prote

## ALIGNMENTS

R.Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy\* A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: B72704

hypothetical protein APE1049 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jul-2004
C;Accession: B72704

B72704

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A;Accession.
A;Ktatus: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <KAW>
A;Residues: 1-493 <KAW>
A;Cross-references: UNIPROT:Q9YD63;
A;Cross-references: Strain KI
                                                                                                                                                                                                                                                           RESULT 2
C85713
                                                  A;Molecule type: DNA
A;Residues: 1-103 <STO>
A;Residues: 1-103 <STO>
A;Cross-references: UNIPROT:Q8X549; GB:AE005174; NID:g12515046; PIDN:AAG56167.1; GSPDB:Carretimental source: strain O157:H7, substrain EDL933
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                                                A;Gene: 22097
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Best Local S
Matches 9
Query Match 41.9%;
Best Local Similarity 47.1%;
Matches 8; Conservative
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Score 52; DB
Pred. No. 1.4;
3; Mismatches
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Pred. No.
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                     DB 2;
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 6;
                       Length 103;
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 Indels
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 Gaps
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K.; Apodaca,
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A;Introns: 9/3; 255/1
A;Introns: 9/3; 255/1
C;Superfamily: helix-destabilizing protein; ribonucleoprotein
F;24-90/Domain: ribonucleoprotein repeat homology <RRM1>
F;24-90/Domain: ribonucleoprotein repeat homology <RRM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q22037; EMBL:S43152
R;Du, Z.; Scheet, P.; Andrews, S.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid F42A6.
                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AF038613; PIDN:AAB92051.1; GSPDB:GN00022; A;Experimental source: strain Bristol N2; clone F42A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Iwasaki, M.; Okumura, K.; Kondo, Y.; Tanaka, T.; Igarashi, H.
Nucleic Acids Res. 20, 4001-4007, 192
A;Title: cDNA cloning of a novel heterogeneous nuclear ribonucleoprotein gene homologue
A;Reference number: S35500; MUID:92375684; PMID:1354852
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A;Gene: ECs2201
                                                                                                                                                                                                                                                                                                             A; Gene: CESP: F42A6.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-346 < IWA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heterogeneous ribonuclear particle protein homolog - Caenorhabditis elegans N;Alternate names: heterogeneous nuclear ribonucleoprotein homolog C;Species: Caenorhabditis elegans
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-346 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Description: The sequence of C.A,Reference number: Z21201
A,Accession: T32620
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A; Residues: 1-103 <HAY>
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                                                                                                                                                                      115-181/Domain: ribonucleoprotein repeat homology
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                                                                                                                         Query Match
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Best Local 9
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                                                               l Similarity
7; Conserv
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8; Conserv
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                                                                                           40.3%;
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                                                               Score 50; DB
Pred. No. 10;
2; Mismatches
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Pred. No.
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                                                               Gaps
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unknown protein encoded within prophage CP-933U [imported] - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: A85821 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K. Nature 409, 529-533, 2001 Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                   RESULT
A85821
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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90973
                                                                                                                                                                                                                                                                                                                                                            R;Hayashi, T.; Makino, I
gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ECs2757 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E99973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SCOEDB:SC5F2A.15
C;Superfamily: enoy1-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA
F;321-605/Domain: 3-hydroxyacyl-CoA dehydrogenase homology <HCD>
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                                                                                                                                                              A;Gene: ECs2757
                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8X4V0; GB:BA000007; PIDN:BAB36180.1; A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-103 <HAY>
                                                                                                                                                                                                                                                                               A; Status: preliminary
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A; Residues: 1-726 <OLI>
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C; Species: Streptomyces coelicolor
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                                                                                 Matches
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Best Local
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nes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 39.5%;
Similarity 44.4%;
8; Conservative
                                  GSWSHPQFEK 20
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Yasunaga, T.; Kuhara,
                                                                            Conservative
24
                                                                                                37.9%;
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Pred. No.
                                                                                                Score 47; 1
Pred. No. 7
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                                                                            Mismatches
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31;
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M.; Shinagawa,
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D.J.; K.; A

Apodaca,

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C;Superfamily: membrane-bound alcohol dehydrogenase, cytochrome c sul
C;Keywords: chromoprotein; heme; iron; metalloprotein
F;58,61/Binding site: heme (Cys) (covalent) #status predicted
F;62/Binding site: heme iron (His) (axial ligand) #status predicted
F;204,207/Binding site: heme (Cys) (covalent) #status predicted
F;204/Binding site: heme (Cys) (covalent) #status predicted
F;336,339/Binding site: heme (Cys) (covalent) #status predicted
F;340/Binding site: heme iron (His) (axial ligand) #status predicted
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residuse; 1-103 <STO>
A;Cross-references: UNIPROT:Q8X4V0; GB:AE005174;
A;Experimental source: strain 0157:H7, substrain
                  A; Title: The Genome of the Natural Genetic A; Reference number: AB2577; MUID:21608550; A; Accession: AH2925
                                                                                   A; Authors: Yoo, H.; ster, E.W.
                                                                                                                                                                      C;Accession: AH2925
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; I
                                                                                                                                                                                                                                  hypothetical protein Atu3006 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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A;Cross-references: UNIPROT:Q9I3C1; GB:AE004588;
A;Experimental source: strain PAO1
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Nature 406, 959-964, 2000
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                                                                                                                                 ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable cytochrome c PA1600 [imported] - Pseudomonas aeruginosa (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: Z3120
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Status: preliminary
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Best Local :
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                                                                                                          Tao,
                                                                                                          Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%;
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                     Agrobacterium tumefaciens (strain
                                           Engineer Agrobacterium tumefaciens C58 PMID:11743193
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34;
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                                                                                                                                                                          ; Chen, L.; Wood, G.E.; Chen, Kutyavin, T.; Levy, R.; Li, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE004091; NID:g9947563; PIDN:AAG0498
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A.; Larbig,
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K.; Lim,
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C;Date: 31-Mar-1988 #sequence revision 31-Mar-1993 #text_change 09-Jul-2004 C;Accession: A26596; S51442; A23444; S43051; S47990 R;Broek, D.; Toda, T.; Michaeli, T.; Levin, L.; Birchmeier, C.; Zoller, M.; Cell 48, 789-799, 1987 Cell 48, 789-799, 1987 A;Title: The S. cerevisiae CDC25 gene product regulates the RAS/adenylate CA;Reference number: A26596; MUID:87131091; PMID:3545497 A;Accession: A26596
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                                       A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1599 <PAU>
A;Residues: 1-1599 <PAU>
A;Cross-references: EMBL:U17247; NID:9577216; PIDN:AAB67360.1; PID:9577222; GSPDB:GN0001
A;Cross-references: EMBL:U17247; NID:9577216; PIDN:AAB67360.1; PID:9577222; GSPDB:GN0001
A;Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.
B;Camonis, J.H.; Kalekine, M.; Gondre, B.; Garreau, H.; Boy-Marcotte, E.; Jacquet, M.
EMBO J. 5, 375-380, 1986
                                                                                                                                                                     A;Description: The sequence of A;Reference number: S51437
                                                                                                                                                                                                   submitted to the EMBL Data Library, November A; Description: The sequence of S. cerevisiae
                                                                                                                                                                                                                                                R;Pauley,
                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1589 <BRO>
A;Cross-references: UNIPROT:P04821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell division control protein CDC25 - yeast N;Alternate names: protein L2142.6; protein C;Species: Saccharomyces cerevisiae
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A; Residues: 1-472 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Goodner, B.; Hinkle, G.; Gattung, A.; Liu, F.; Wollam, C.; Allinger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein AGR_L_3586 [imported] - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct.-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-C;Accession: F98356
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A; Title: Characterization, cloning and sequence analysis A; Reference number: A23444; MUID:86220116; PMID:3011405
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Pred. No. 37;
2; Mismatches
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                                                                                                                                                                                                                                                                     EMBL:M15458; NID:g171184;
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ckelz, B.,
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A;Cross-references: EMBL:X03579
C;Genetics:
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A;Genetics:
A;Genetics:
A;Gross-references: SGD:S0004301; MIPS:YLR310c
A;Cross-references: SGD:S0004301; MIPS:YLR310c
A;Map position: 12R
C;Function:
A;Map position: positive control of level of cellular cAMP at the stage at which the cell
A;Description: positive control of level of cellular cAMP at the stage at which the cell
C;Superfamily: budding yeast CDC25; CDC25-type guanine nucleotide exchange activator hom
C;Superfamily: budding yeast CDC25; CDC25-type guanine protein
C;Keywords: cell bycle control, transmembrane protein
F;65-123/Domain: bH3 homology <SH3>
F;1301-1542/Domaih: CDC25-type guanine nucleotide exchange activator homology <SOS>
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A;Accession: S43051
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A;Residues: 1-496,'Y',498-953,'LSVIMNLSR',964-1589 <CAM>
A;Cross-references: EMBL:X03579; NID:g3483; PIDN:CAA27259.1; PID:g3484
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A;Title: Determination of the coding capacity of the BamHI DNA fragment A;Reference number: A48560; MUID:93070559; PMID:1332274
A;Accession: C48560
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F90197
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A;Residues: 1-233 <ROS>
A;Cross-references: UNIPROT:P36297
A;Note: sequence extracted from NCBI backbone
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A;Reference number: A99139
A;Accession: F90197
A;Status: preliminary
                                                                  C;Accession: F90197
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Al Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                 hypothetical protein SSO0519 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
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Matches 7
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Residues: 877-1589 <DAN>
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9; Conserv
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Pred. No.
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                                                                                                                                                                     Y.; Allard, G.; Awayez,
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                                                                                                                                                X.; Thi-Ngoc, H.P.; Redder,
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A;Molecule type: DNA
A;Residues: 1-243 <KUR>
A;Cross-references: UNIPROT:Q9UWS5; GB:AE006641; NID:g13813677; PIDN:AAK40837.1;
C;Genetics:
A;Gene: SSO0519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: sequence extracted from NCBI backbone (NCBIN:76628, NCBIP:76629)

R;Kim, Y.J.; Baker, B.S.

MOI. Cell. Biol. 13, 174-183, 1993

A;Title: Isolation of RRM-type RNA-binding protein genes and the analysis of their A;Reference number: A48110; MUID:93109300; PMID:8417324

A;Accession: G48110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Matunis, E.L.; Matunis, M.J.; Dreyfuss, G.
J. Cell Biol. 116, 257-269, 1992
A;Title: Characterization of the major hnRNP proteins from A;Reference number: A41732; MUID:92112968; PMID:1730754
A;Accession: D41732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 02-Aug-1994 #text_change 16-Aug-2004
C;Accession: D41732; G48110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: FlyBase:FBgn0001215; FlyBase:FBgn0010261
C;Superfamily: ribonucleoprotein repeat homology
F;8-74/Domain: ribonucleoprotein repeat homology <RRM1>
F;97-163/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:S51720; NID:g262267; PIDN:AAB24628.1; A;Note: sequence extracted from NCBI backbone (NCBIN:121150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 10-53 < KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-385 < MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary
A;Nolecule type: mRNA
A;Nolecule type: mRNA
A;Residues: 1-1885 <5AT>
A;Cross-references: UNIPROT:P54891; GB:D14996; NID:g434059; PIDN:BAA03641.1; PID:g453240
A;Cross-references: UNIPROT:P54891; GB:D14996; NID:g434059; PIDN:BAA03641.1; PID:g453240
A;Cross-references: UNIPROT:P54891; GB:D14996; NID:g434059; PIDN:BAA03641.1; PID:g453240
                                                                                                                                   C;Accession: JQ2183
R;Sato, K.; Yoshikawa, N.; Takahashi, T.
J. Gen. Virol. 74, 1927-1931, 1993
A;Title: Complete nucleotide sequence of the genome of an apple isolate
A;Reference number: JQ2183; MUID:93389448; PMID:8376968
A;Reference number: JQ2183; MUID:93389448; PMID:8376968
                                                                                                                                                                                                                              hypothetical 216.5K protein - apple chlorotic leaf spot virus (isolate P-205) N;Alternate names: ORF 1 protein C;Species: apple chlorotic leaf spot virus C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004 C;Accession: JQ2183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: FlyBase: Hrb98DE; FlyBase: Rbp7
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77.8%;
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Pred. No. 26;
1; Mismatches

    fruit fly (Drosophila melanogaster)

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Pred. No.
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NCBIP: 121151)
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Qy 1 WSHPQFEKGGGSWSHP 16	C;Keywords: ATP  Query Match 37.1%; Score 46; DB 2; Length 1885; Best Local Similarity 43.8%; Pred. No. 2.3e+02; Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps
	0;

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                 49.5
                                                                                                                                                                                                   UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     March 2, 2005, 12:20:44; Search time 74.3089 Seconds (without alignments)
137.824 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
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   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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QBA6Y2
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06pbw7
08pbw7
09mam2
095x69
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092889
022037
098312
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081w8
081rf3
09mcn2
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Q8ch90
Q9ch90
Q9m63
Q8a6y2
Q8pn18
Q7pp48
Q7pp48
Q72iw0
Q8x51w0
Q8x51w0
Q8x51w0
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Q8x51w0
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2 arabidopsis
5 caenorhabdi
7 caenorhabdi
9 rhizobium m
0 mus musculu
2 geobacillus
8 brachydanio
0 oryza sativ
3 rhodopirell
2 bacteriopha
8 streptomyce
4 oryza sativ
1 burkholderi
7 burkholderi
6 homo sapien
4 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                 3 aeropyrum p
2 bacteroides
8 bradyrhizob
8 anopheles g
2 porphyromon
0 thermus the
                                                                                                                                                                                                                                                                                                2 arabidopsis
8 drosophila
1 drosophila
                                                                                                                                                                                                                                                                   oryza sativ
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xanthomonas
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Regult No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32
47	47	47	47	47	47	47	47.5	47.5	47.5	47.5	47.5	47.5	48
37.9	37.9	37.9	37.9	37.9	37.9	37.9	38.3	38.3	38.3	38.3	38.3	38.3	38.7
508	472	433	259	228	159	103	848	841	828	462	237	226	843
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MATK_MARSC	QBUBLO	Q913C1	PRIO_TRIVU	Q9D1N2	Q7QK59	Q8X4V0	Q8ZRR6	Q86VX7	SOX6_HUMAN	097643	Q866U8	Q866W0	Q6CKE4
Q8wkk9 marathrum s	Q8ubl0 agrobacteri	Q9i3c1 pseudomonas	P51780 trichosurus	Q9dln2 m mus muscu	Q7qk59 anopheles g	Q8x4v0 escherichia	Q8zrr6 salmonella	Q86vx7 homo sapien	P35712 homo sapien	097643 lama glama	Q866u8 tenrec ecau	Q866w0 myotis dauk	Q6cke4 kluyveromyc

# ALIGNMENTS

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ULT 2  H90  GBCH90  PRELIMINARY;  PRT; 743 AA.  QBCH90;  O1-MAR-2003 (TrEMBLrel. 23, Created)  O1-MAR-2003 (TrEMBLrel. 23, Last sequence update)  O1-MAR-2004 (TrEMBLrel. 26, Last annotation update)  Soluble guanylyl cyclase alpha 2 subunit E219G mutant.  Rattus norvegicus (Rat).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus.  NCBI TaxID=10116;  SEQUENCE FROM N.A.  TISSUB-Kidney;  Nakamura I., Yao Y., Suzuki N.;	Query Match 49.2%; Score 61; DB 2; Length 704; Best Local Similarity 100.0%; Pred. No. 3.4; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps  , 11 GSWSHPQPEK 20	QBCJD2 QBCJD2 QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCJD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QBCD2; QB

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R SMART; SM00044; CYCc; 1.
R SMART; SM00044; CYC; 1.
R PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
R PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.
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01-NOV-1999
                                                                                                                                                                                               GO; GO:0005381; F:iron ion transporter activity; IEA.
GO; GO:0006827; P:high affinity iron ion transport; IE;
InterPro; IPR002491; Peripla BP.
InterPro; IPR002913; Prefoldin.
InterPro; IPR002917; Spectrin.
InterPro; IPR019978; trNA binding_arm.
Pfam; PF01497; Peripla BP 2; 1.
Complete proteome; Hypothetical protein.
SEQUENCE 493 AA; 52685 MW; 9AA07ED93055826E CRC64;
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Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Ko Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6.83-101(1999)
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STRAIN=K1;
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NCBI_TaxID=56636;
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                                                 WSHPQFEKGGGSWSHPQFE 19
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                                                                                                      Conservative
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                                                                                                                          Score 58; DB Pred. No. 6.1;
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RESULT 4 Q8A6Y2

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RESULT 5
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II Bradyrhizobium japonicum USDA110.";

DNA Res. 9:189-197(2002).

REMEL; AP005949; BRC49085.1; ---
RG0; G0:0005489; F:elactohol debydrogenase activity; IEA.
RG0; G0:0005489; F:electron transporter activity; IEA.
RG0; G0:0005489; F:oxidoreductase activity; IEA.
RG0; G0:0016491; F:oxidoreductase activity; IEA.
RG0; G0:0016491; F:oxidoreductase activity; IEA.
RG0; G0:0016491; F:oxidoreductase activity; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
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RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
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RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; P:electron transport; IEA.
RG0; G0:0006118; R0:0006118;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches
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STRAIN-VPI-5482 / ATCC 29148;

STRAIN-VPI-5482 / PubMed=12663928; DOI=10.1;

MEDLINE=22550858; PubMed=12663928; DOI=10.1;

Xu J., Bjursell M.K., Himrod J., Deng S., Cc
Chiang H.C., Hooper L.V., Gordon J.I.;

"A genomic view of the human-Bacteroides the
Science 299:2074-2076(2003).

EMBL; AE016933; AA076850.1; -..

GO; GO:003824; F:catalytic activity; IEA.
InterPro; IPR001087; Lipase GDSL.

Pfam; PF00657; Lipase GDSL; 1.
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Q89NL8;
01-JUN-2003 (TrEMBLrel. 2
01-JUN-2003 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
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Tabata S.
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Q8A6Y2;
01-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OrderedLocusNames=bll3820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22484998; PubMed=12597275;
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STRAIN=USDA110;
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Bacteria; Bacteroidetes; Bacteroides
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OrderedLocusNames=BT1743;
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01-OCT-2003
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8; Conserv
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507 AA; 56254 MW; I
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PubMed=12663928; DOI=10.1126/science.1080029;
V Himrod J., Deng S., Carmichael L.K.,
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Bradyrhizobium.
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Pred. No. 12;
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B2B890D937A1E78A CRC64;
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N [1]

P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

C STRAINE-82867; PubMed=12949112;

RX MEDLINE-22867; PubMed=12949112;

RX Pol-10.1128/JB.185.18.5591-5601.2003;

RA Nelson K.E., Fleischmann R.D., DeBoy R.J., Durkin A.S., Gwinn M.L.,

RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,

RA Haft D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray

Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

Granger C.M.;
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Ol-MAR-2004 (TrEMBLrel. 26, Last sequence update)

Ol-MAR-2004 (TrEMBLrel. 26, Last sequence update)

Edycline cleavage system protein.

Name=gcvP, OrderedLocusNames=PG1305;

Porphyromonas glingivalis (Bacteroides gingivalis).

Bacteria, Bacteroides Bacteroides (class); Bactero
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Best Local S
Matches 9
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Best Local S
Matches 7
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Q7MV12;
01-MAR-2004 '(TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
01-MAR-2004 (TrEMBLrel. 2
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Q7PP48;
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01-MAR-2004 (TrEMBLrel. 26, La

01-MAR-2004) (TrEMBLrel. 26, La

ENSANGPO0000013599 (Fragment).

Name=ENSANGG00000011110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anopheles Génome Sequencing Consortium,
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-I- CAUTION; The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=PEST;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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ProDom; PD011584; CytC_adh; 2.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 3.
PROSITE; PS0030; RRM_RNP_1; UNKNOWN_1.
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AAAB01008960; E
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Pred. No.
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Pred. No.
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(class); Bacteroidales;
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Matches 8
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EMBL; AE017304; AAS81363.1; -.

GO; GO:016740; F:transferase activity; If
InterPro; IPR002110; ANK.
InterPro; IPR011023; Nop2p.
InterPro; IPR016174; NusB_region.
PR1NTS; PR01415; ANKURIN.
ProDom; PD005242; NusB_region; 1.
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Liesegang H., Johann A., Lienard T., Gohl O., Marti
Jacobi C., Starkuviene V., Schlenczeck S., Dencker
Klenk H.-P., Kramer W., Merkl R., Gottschalk G., Fri
"The genome sequence of the extreme the themophilus.";
Nat. Biotack
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TIGR; PG1305; -.
TIGR; GG0:0005561; C:glycine dehydrogenase complex (decarboxylat...
GO; GO:0004375; F:glycine dehydrogenase (decarboxylating) act...
GO; GO:0006544; P:glycine metabolism; IEA.
InterPro; IPR003437; GDC-P.
Pfam; PF02347; GDC-P; 1.
TIGRPANs; TIGR00461; gcvP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the ora Porphyromonas gingivalis strain W83. J. Bacteriol. 185:5591-5601(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
PubMed=15064768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus thermophilus (strain HB27 / ATCC BAA-163 / DSI
Bacteria; Deinococcus-Thermus; Deinococci; Thermales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OrderedLocusNames=TTC1021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=262724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGRFAMs;
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447 AA;
                                                                                                                                                                                                                                                                                                                 WPHRLEGEGHFLARFRKEGGAWSTPRLER
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                                                                                                                                                                                                                                                                                                                                                                                      WSH-----
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proteome; Transferase.
447 AA; 48704 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No.
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Pred. No. 24;
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Q8X549 PRELIMINARY; Q8X549; Q7ADVO; 01-MAR-2002 (TIEMBLIEL: 1 01-MAR-2002 (TIEMBLIEL: 25-OCT-2004 (TIEMBLIEL: 1

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Created)
Last sequence update)
Last annotation updat

PRELIMINARY;

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EP SEQUENCE FROM N.A.

CSTRAIN=306 / ATCC 13902 / XV 101;

CSTRAIN=306 / ATCC 13902 / XV 101;

WMEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A da Silva A.C.R., Ferro J.A., Reinach F.C., Carah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluya M.A., Almeida N.F.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluya M.A., Ciapina L.D.,

Ciamarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.D.,

A Camarotte G., Connavan F., Cardozo J., Chambergo F., Ciapina L.D.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

A Camarotte G., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

A Carail J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

A Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,

A Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

A Katsuyama A.M., Kishi L.T., Lette R.P., Lemos B.G.M., Jemos M.V.F.,

A Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

AN Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

AN Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
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Best Local S
Matches 8
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
Nolybdopterin-converting factor chain 2.
Name=moaE; OrderedLocusNames=XAC1100;
Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli

0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).
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STRAIN-0157:H7 / EDL933 / ATCC 700927 / EHEC;

MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller I.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonadaceae;
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EMBL; AP002557; BAB5624.1; -.
PIR; A90904, A90904.
PIR; C85713; C85713.
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SEQUENCE 103 AA; 11980 MW; 5A42AAF91CF29EB6 CRC64;
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STRAIN=0157:H7 / R
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Tobe T.,
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O71D58;
O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update
O5-JUL-2004 (TrEMBLrel. 27, Last annotation upda
CG13011 (Fragment).
Drosophila yakuba (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insect
Neoptera; Endopterygota; Diptera; Brachycera; Mu
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                   Matches
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Best Local
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Best Local :
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Q9LVU2;
01-OCT-2000
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SEQUENCE
                                                                                                                                                                                                                                                                                                             features clones.";
                  NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheor Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=20181125; Sato S., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 146 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 417:459-463(2002).
EMBL; AE011739; AAM35974.1;
HSSP; P30749; 1FM0.
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                                                                                                                                                                                                                                                                                                                         "Structural
features of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Comparison of the genomes of two Kanthomonas pathogens with differing host specificities.";
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NCE 150 AA; 16928 M
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Y., Kaneko T., Katoh
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RX MEDLINEZ FROM N.A.

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., if P.M., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Sulton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazed R.G., Champe M., Pfeiffer B.D.,

RA Mann K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Maril J.F., Agbayani A., An H.J., Andrews-Fennkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouke J., Davise P.,

RA Borkova D., Botchan M.R., Bouke J., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibeywam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Wilshina N.V., Mobarry C., Morris J., Moshrefi A.,

Monto S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelsen D.L.,

RA Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Syler B., Spradling A.C., Stapleton M., Stopg R., Sun E.,

RA Syler E., Spradling A.C., Stapleton M., Stopg R., Shu K.,

RA Shue B.
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Matches 8
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01-MAY-2000
01-OCT-2003
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"An evolutionary analysis of orphan Genome Res. 13:2213-2219(2003).
EMBL; AF532012; AA(09911.1; -.
GO; GO:0016020; C:membzane; IEA.
InterPro; IPR008253; Marvel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly)
Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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NCBI_TaxID=7227
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8; Conserv
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Last annotation update)
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Pred. No. 20;
2; Mismatches
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Q654S7; Q654S7; 25-OCT-2004 25-OCT-2004 25-OCT-2004

PRELIMINARY;

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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein B1135C02.12 (Hypothetical prot
OSJNBa0011P19.40).
Name=B1135C02.12; Synonyms=OSJNBa0011P19.40;

Oryza sativa (japonica cui Eukaryota; Viridiplantae;

cultivar-group). ae, Streptophyta, Embryophyta, Tracheophyta, ophyta, Liliopsida, Poales, Poaceae,

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RESULT
Q65487
ID Q6AC
AC
DT 255
DT 255
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                                                                                                                                                                                                                                                                                                                                   Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E. Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kaminker J.S., Bergman C.M.
Patel S., Frise E., Wheeler
Ashburner M., Celniker S.E.
"The transposable elements
a genomics perspective.";
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MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                           InterPro; IPRO
Pfam; PF01284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Annotation of the Drosophila melanogaster euchromatic genome:
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                                                                                                                                                                                           WLHPOFLVRPGFWAYP 145
                                                                                                                                                                                                                    WSHPQFEKGGGSWSHP 16
                                                                                                                                                                                                                                                                                                                        IPR008253; Marvel.
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                                                                                                                                                                                                                                                                                                19460 MW;
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Ehrhartoideae; Oryzeae; Oryza. NCBI\_TaxID=39947;

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RX MEDIJINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RX MEDIJINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

RX MEDIJINE=22022145; PubMed=12024217; DOI=10.1038/417459a;

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A Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,

A Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,

A Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,

A Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,

Ikeno M., Itoh S., Itoh T., Itoh Y., Itoh Y., Irabuchi A., Kamiya K.,

Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,

A Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,

A Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,

AN Nagasaki N., Negishi M., Ohta I., Oho N., Saji S., Sakai K., Shibata M.,

AN Namiki N., Negishi M., Ohta I., Oho N., Saji S., Sakai K., Shibata M.,

AN Namiki N., Wangata H., Yamane H., Yoshiki S., Sakai K., Tsuji K.,

AN Waki K., Yamagata H., Yamane H., Yoshiki S., Sokai K., Tsuji K.,

AN Yano M., Jiang J., Gojobori T.,

"The genome sequence and structure of rice chromosome 1.";

"The genome sequence and structure of rice chromosome 1.";

BMBL; AP004358; BAD45690.1; -.

BMBL; AP003211; BAD45055.1; -.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Molybdopterin-converting factor chain 2.
Name=moaE; OrderedLocusNames=XCC0999;
Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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Hypothetical protein.
SEQUENCE 55 AA; 53
                                             Nature 417:459-463(2002).
EMBL; AE012196; AAM40300.1; -.
HSSP; P30749; INVJ.
                                                                                                                                                                                Setubal J.C., Kitajima J.P.;
"Comparison of the genomes of two
host specificities.";
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Pfam; PF02391; MoaE; 1.
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53.5	53.5	53.5	53.5	55	57	57	57	57	57	58	58	58	58	58	58	58	58	82	58
43.1	43.1	43.1		44.4	46.0	46.0	46.0	46.0	46.0	46.8	46.8	46.8		46.8	46.8	46.8	46.8	46.8	46.8
268	268	268	267	633	67	67	19	19	10	763	661	539	539	258	258	209	183	183	19
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ADR70386	ADR70319	ADR70385	ADR70320	ADS20255	ABM44441	AAU47922	ADI39157	ABG74882	ABP56623	ADB85492	AAE38369	ADI39158	ABG74883	ADA00702	ADA27293	ADA00709	ADA00703	ADA27294	ADI39156
Adr70386 Polioviru	Adr70319 Polioviru	Adr70385 Polioviru	Adr70320 Polioviru	Ads20255 Human agg	Abm44441 Propionib	Aau47922 Propionib	_	Abg74882 Bacteriop	Abp56623 C-termina	Adb85492 Human agg	Aae38369 Human agg	Adi39158 Enterobac	Abg74883 Bacteriop	Ada00702 Modified	Ada27293 Plasmid p	Ada00709 Modified	Ada00703 Modified	Ada27294 Plasmid p	Adi39156 Construct

# ALIGNMENTS

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least two high-affinity streptavidin	New isolated peptide, useful as affinity purification tag for recombinant	WPI; 2003-031166/03.	Schmidt T;	(BIOA-) INST BIOANALYTIK GMBH GOETTINGEN.	21-MAR-2001; 2001DE-01013776.	21-MAR-2001; 2001DE-01013776.	02-OCT-2002.	DE10113776-A1.		kegion 9i2 /label≡ GGGS repeat	region 920 /note= "GGGS repeate 2-5 optionally absent, residues 13-	Symthetic.	Streptavidin; protein chip; microtitre plate; detection.	Streptavidin binding peptide SEQ ID NO 11.	28-MAR-2003 (first entry)	ABP60370;	ABP60370 standard; peptide; 36 AA.	T 1 370

Claim 8; Page 16; 18pp;

German.

The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing a least one motif His-Pro-X where x = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides

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RESULT 2
ABP60362
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The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-x where x = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein as (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated peptide, protein, comprises at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-031166/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 4; 18pp; German
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9. .16
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Sequence 24

RESULT 4 ABP60369

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Matches 15; Conserv
                                                                                                                                                                                                                                                     This invention describes novel polypeptides (I) that are muteins of bilin -binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being used as label. Compared with Dig-specific antibodies, (I) have a simpler structure and are easier to prepare. They have very high specificity for Dig, relative to other steroids, and fusion partners may be attached to either end without compromising their ability to bind
                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; Page 72-74; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
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                                                                                                                     Length 659;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Prox where x = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein as (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                   Human NOVX polypeptide, NOV2f
                                                                     23-SEP-2004
                                                                                                                  ADP87577;
                                                                                                                                                               ADP87577 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 16; 18pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein, comprises at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-031166/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MAR-2001; 2001DE-01013776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001; 2001DE-01013776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptavidin; protein chip; microtitre plate; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptavidin binding peptide SEQ ID NO 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOA-) INST BIOANALYTIK GMBH GOETTINGEN
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                        1 WSHPQFEKGGGS--------WSHPQFEK 20
                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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9. .27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= unknown
/note= "optionally deleted for 1-15 residues"
                                                                                                                                                             protein; 772
                                                                                                                                                                                                                                                                                                                                                                                                     52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as affinity purification tag for recombinant least two high-affinity streptavidin-binding
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 65.5; DB (
Pred. No. 0.098;
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PAFSHGGFSHNWSHPQFEK 772 POFEKGGGS--WSHPQFEK 20 Query Match
Best Local Similarity
Matches 13; Conserv

Conservative

<u>,</u>

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Gaps

1;

51.6%;

Score 64; DB 8; Pred. No. 4.1; Mismatches

Length 772; Indels

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CC comprising any of the amino acid sequences cited above; a method for antibody that immunospecifically binds to the target polypeptide, where the target polypeptide comprises any of the above-mentioned amino acid sequence that is at least 95% identical to the sequences, an amino acid sequence that is at least 95% identical to the above-mentioned amino acid sequence of at least one domain of the above-mentioned amino acid sequences, or an amino acid sequence that is at least 95% identical to the domain of the above amino acid sequence of a treatment of a pathology, where the pathology is related to aberrant capression or aberrant physiological interactions of a target polypeptide and a method of screening for a modulator of acid to apathology where the pathology is related to aberrant capression or aberrant physiological interactions of a target polypeptide or predisposition to a pathology associated with a target polypeptide. The modulating compounds have anorectic and antidiabetic activities. The mucleic acid sequences of the invention may be used in gene therapy to treat disorders. The proteins of the invention may be used in creating a vaccine. The composition and methods are useful for identifying compounds that modulate protein activity or for diagnosing, preventing or treating compounds to the treating compounds are also used as hybridization probes, in chromosome mapping, tissue typing, preventive medicine, and of the invention and beauty protein activity or proventive medicine, and compounds in the modulation of the sequence represents a NOVX polypeptide of the invention and probes, in the modulation of the sequence represents a NOVX polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2002;
20-DEC-2002;
20-DEC-2002;
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28-OCT-2002;
31-OCT-2002;
13-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel isolated nucleic acid molecule comprising any of the nucleotide sequences (e.g. 3614, 2127 or 2120 base pairs) fully defined in the specification; or encodes any of the amino acid sequences (e.g. 698, 702 or 709 amino acids) fully defined in the specification. The invention further comprises: an isolated polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anorectic; antidiabetic; gene therapy; vaccine; obesity; diabetes; insulin resistance; hybridization probe; chromosome mapping; tissue typing; preventive medicine; pharmacogenomics; NOVX; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 32; 570pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New NOVX nucleic acid molecules and polypeptides useful for preventing treating NOVX-associated disorders, e.g. diabetes, insulin resistance cobesity, and in chromosome mapping, tissue typing or pharmacogenomics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADP87576.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-2003; 2003WO-US034114.
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Sequence 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2002US-0421239P.
; 2002US-0421700P.
; 2002US-0422776P.
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; 2002US-0435568P.
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                                                         disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAMTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAMTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The protein of the invention demonstrates osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of the human aggrecanase ADAMTS4 mutant E362Q protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity for treating aggrecanase-associated conditions, including osteoarthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADS20243 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004011637<sup>L</sup>A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to a novel isolated, modified ADAMTS4
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FREEMAN B A.
GEORGIADIS K I
LAVALLIE E R.
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eorgiadis KE,
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Lavallie ER;
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Sequence, 845

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Best Local Similarity
Matches 11; Conserv
This invention describes the preparation of anticalins from polypeptides of the lipocalin family by mutation of amino acids in the region of the 4 peptide loops (at one end of the cylindrical 'leaflet' structure'). Anticalins can bind to a predetermined ligand with determinable affinity. Anticalins or fusions of anticalins, are used: (a) when immobilized, for separation; and (b) when labeled, for identification of ligands (or their fusions or conjugates). Typically they bind to tissue- or tumor specific surface molecules and can be used for tumour analy or directly for tumour therapy. Mutations can be introduced into lipocalin polypeptides more easily than into antibodies, since lipocalin polypeptides have only 4 (contrast 6) sequence segments. The peptide loops can tolerate amino
                                                                                                                                                                                      New anticalins produced by mutation of lipocalin family protein
                                                                                                                                                                                                                               WPI; 1999-255093/21.
                                                                                                                                                                                                                                                        Skerra A,
                                                                                                                                                                                                                                                                                                                                    25-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipocalin; anticalin; peptide loop; leaflet structure; antibody; therapy; tissue-specific surface molecule; tumour-specific surface molecule; tumour imaging; bilin binding protein; phage coat protein pIII.
                                                                                                                                                                                                                                                                                                            26-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid pBBP20 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW93966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW93966 standard; protein;
                                                                                                                                                                                                                                                                                  (SKER/) SKERRA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 WSHPQFEKAGG-W 531
                                                                                                                                                                                                                 AAX24099.
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                                                                                                                                                                                                                                                        Beste G,
                                                                                                                                                             Page 67-69; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                          97DE-01042706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "This fusion peptide is constructed binding protein, a strep-Tag II region and phage coat protein pIII"
                                                                                                                                                                                                                                                                                                                                                                                                                         207
                                                                                                                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Bilin binding protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label=
                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .195
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                                                                                                                                                                                                                                                        Schmidt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                              "phage coat protein pIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Strep-Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fusion_peptide
                                                                                                                                                                                                                                                        '7
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                                                                                                                                                                                                                                                                                                                                                                                                                                       by TAG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   II region"
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a fragment
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RESULT 8
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Matches 12
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Best Local
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                                                                                                                                                                                                                  This invention describes novel polypeptides (1) that are muteins of bilin binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (1), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecules, other biological or synthetic macromolecules or low
                                                                                                                                                                                                                                                                                                                                                                                       New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for digoxigenin;
                                                                                                        Sequence 396 AA;
                                                                                                                                                molecular weight compounds, particularly in assays where Dig is being used as a label. Compared with Dig-specific antibodies, (1) have a simpler structure and are easier to prepare. They have very high specificity for Dig, relative to other steroids, and fusion partners to a trached to either end without compromising their ability to bind be attached to either end without compromising their ability to bind
                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 55-56; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-071071/08.
N-PSDB; AAF25695.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JUN-1999; 99DE-01026068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUN-2000; 2000WO-DE001873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bilin-binding protein; mutein; BBP; digoxigenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bilin binding-protein associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB46420 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid changes without significant effect on folding. Anticalins have high specific affinity, comparable with that for antibodies. This sequence represents a fusion polypeptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200075308-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SKER/) SKERRA A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198
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                                             l Similarity
12; Conser
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WSHPQFEK--GGGS 12
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                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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85.7%;
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                                             Score 62; DB
Pred. No. 3.8;
0; Mismatches
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Pred. No.
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                                                                         DB 4;
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                                                                         Length 396;
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RESULT 10
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Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB46423 standard;
 Plasmid pHNGAL5 fragment protein
                             20-NOV-2003
                                                       ADA27291;
                                                                                                                                                                                                                                                            Sequence 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Skerra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bilin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bilin binding-protein associated protein #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB46423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 62-64; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-1999;
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                                                                                 ADA27291 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SKER/) SKERRA A.
                                                                                                                                                    198
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                                                                                                                                                                                                        12;
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                                                                                                                                                                   1 WSHPQFEK--GGGS 12
                                                                                                                                                                                                                   Similarity
                                                                                                                                                    WSHPQFEKXAGGGS
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                                                                                                                                                                                                        Conservative
                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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                                                                                 protein;
                                                                                                                                                                                                                   50.0%;
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                                                                                 400 AA
                                                                                                                                                                                                       Score 62; DB
Pred. No. 3.8;
0; Mismatches
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                                                                                                                                                                                                                                DB 4;
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RESULT 11
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Best Local Similarity
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                                                                                                                                                                                                                                The present invention relates to a method for generating muteins of human neutrophil gilatinase-associated lipocalin (NGAL), rat alpha2-microglobulih-related protein (A2m) or mouse 2493/uterocalin, by subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the coat protein pIII of a filamentous bacteriophage of the M13-family of a fragment of the coat protein. The present sequence is the protein encoded by a fragment of plasmid pHNGAL5, used to illustrate the invention. This sequence comprises human hNGAL, a Strep-Tag II and a fragment of phage coat protein pIII.
                                                                                                                                                                                                                                                                                                                                                                                                               Generating a mutein of a protein for validating the protein as drug target by subjecting the protein to mutagenesis at sequence positions corresponding to sequence positions of the human neutrophil gelatinase-associated lipocalin.
  20-NOV-2003
                        ADA27292;
                                                 ADA27292
                                                                                                                                                                                                               Sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mutein; human; neutrophil gelatinase-associated lipocalin; hNGAL; rat; alpha2-microglobulin-related protein; A2m; mouse; 24p3; uterocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001; 2001WO-EP011213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PIER-) PIERIS PROTEOLAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
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DB; ADA27285.
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                                                                                                                                       \vdash
                                                                                                                                 WSHPQFEK--
                                                standard;
                                                                                                              WSHPQFEKQAGGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlehuber
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Page 57-58;
(first
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Tag II and a fragment of phage
22. .199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "OmpA signal sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Strep-Tag II affinity tag"
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                                                protein; 400
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 entry)
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                                                                                                              215
                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                      68pp; English.
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                                                                                                                                                                          Score
Pred.
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RESULT 12
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Best Local :
                                                                                                                                                     Matches
                                                                                                                                                                                                                                             The present invention relates to a method for generating muteins of human neutrophil gelatinase-associated lipocalin (hNQAL), rat alpha2-microglobulin-related protein (A2m) or mouse 2493/uterocalin, by subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the coat protein pIII of a filamentous bacteriophage of the M13-family or for a fragment of the coat protein. The present sequence is the protein encoded by a fragment of plasmid pHNGAL3, used to illustrate the invention. This sequence comprises human hNGAL, a Strep-Tag II and a
ADA00700;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Generating a mutein of a protein for validating the protein target by subjecting the protein to mutagenesis at sequence corresponding to sequence positions of the human neutrophil
                           ADA00700 standard;
                                                                                                                                                                                                          Sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 59-61; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              associated lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADA27286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2003-381639/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutein; human; neutrophil gelatinase-associated lipocalin; hNGAL; rat; alpha2-microglobulin-related protein; A2m; mouse; 24p3; uterocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001; 2001WO-EP011213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-SEP-2001; 2001WO-EP011213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pHNGAL3 fragment protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                  Local Similarity
les 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIERIS PROTEOLAB
                                                                                               WSHPQFEKQAGGGS 215
                                                                                                                       WSHPQFEK--GGGS 12
                                                                                                                                                                                                                                   of phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schlehuber S;
                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Mature protein; fusion protein of hNGAL, Strep-
Tag II and a fragment of phage coat protein pIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Encoded by TAG"
211. .400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "Strep-Tag II affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Mature hNGAL"
                                                                                                                                                                                                                                   coat protein pIII.
                         protein; 400
                                                                                                                                                                 50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Amino acids 217-406 of coat protein pIII"
                                                                                                                                                    0
                                                                                                                                                                 Score 62; DB Pred. No. 3.8;
                                                                                                                                                    Mismatches
                                                                                                                                                                               6
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06-NOV-2003

(first

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The present invention describes a method for generating a mutein of a CC protein selected from a human neutrophil gelatinase-associated lipocalin CC (hNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse CC 2493/uterocalin (24p3), where the mutein has a detectable affinity to a given target, comprising subjecting the protein to mutagenesis at CC positions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in CC muteins of the protein. Also described: (1) a mutein of hNGAL, alm or 24p3 having detectable binding affinity to a given target, obtained by CC the method described above; (2) a fusion protein comprising the mutein of hNGAL, A2m or 24p3, where an enzyme, a protein or a protein domain, a CC peptide, a signal sequence and/or an affinity tag is operably fused to the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein of hNGAL, A2m or 24p3 or the fusion protein of exercised above, and a carrier. The muteins have cytostatic activity, and can be used in CC gene therapy. The method is useful in generating or producing a mutein of hNGAL, A2m or 24p3 or a fusion protein. The mutein of hNGAL, A2m or 24p3 or a fusion protein. The mutein of hNGAL, A2m or 24p3 or the fusion protein is useful in detecting a given target by contacting the mutein of the given target under conditions that allow complex formation between the mutein and the given target, and determining the complexed mutein a portion a mutein of the activity and can be actived.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 94-95; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or mouse 24p3/uterocalin, comprises subjecting the protein to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-372000/35
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16-APR-2002; 2002WO-EP004223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutein, human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-2002; 2002WO-EP010490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA00731.
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croglobulin-related protein; A2m; mouse 24p3/uterocalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "modified hNGAL, Strep-tag II and
protein pIII fragment fusion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label = signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:13
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Best Local S
Matches 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 400 AA;
                               Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or m 24p3/uterocalin, comprises subjecting the protein to mutagenesis.
                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                    Misc-difference 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutein; human neutrophil gelatinase-associated lipocalin; hNGAL; rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin; 24p3; mutegenesis; fusion protein; cytostatic; gene therapy; tumour imaging; cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified hNGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADA00707 standard;
                                                                               N-PSDB;
                                                                                                                Skerra
                                                                                                                                                            27-SEP-2001; 2001WO-EP011213
16-APR-2002; 2002WO-EP004223
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                       (PIER-) PIERIS PROTEOLAB
                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                             2003-372000/35.
DB; ADA00706.
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                                                                                                                Schlehuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related fusion protein
                                                                                                                                                                                                                                                                                                                                                          /note= "modified hNGAL, Strep
protein pIII fragment fusion
                                                                                                                                                                                                                                                                                                                                                                                  22. .400
                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                note= "coat protein pIII fragment 217-406"
                                                                                                                                                                                                                                                                                                             note= "Strep-tag II affinity
                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                       note= "amber stop codon'
                                                                                                                                                                                                                                                                                                                                                                                             label=
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                                                                                                                                                                                                                                                                                                                                    "mature hNGAL"
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Pred. No.
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3.8;
                                                                                                                                                                                                                                                                                                                                                           Strep-tag II and phage coat usion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Disclosure; Page 104-105; 122pp; English

mouse

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CC given target, comprising subjecting the protein to mutagenesis at C positions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in muteins of the protein. Also described: (1) a mutein of hNGAL, A2m or CC 2493 having detectable binding affinity to a given target, obtained by the method described above; (2) a fusion protein comprising the mutein of chNGAL, A2m or 2493, where an enzyme, a protein or a protein domain, a CC peptide, a signal sequence and/or an affinity tag is operably fused to the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the fusion protein described above, and a carrier. The muteinsh have cytostatic activity, and can be used in CC gene therapy. The method is useful in generating or producing a mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or the fusion protein is useful in generating or producing a mutein of conditions that allow complex formation between the mutein and the given target under conditions that allow complex formation between the mutein and the given carget, and determining the complexed mutein by a suitable signal. The conjectile, an organic molecule or a metal complex and the detection is carried out for validation of the protein as a pharmacological drug carget. The mutein may also be used in medicine, e.g. for tumour imaging cor directly for cancer therapy. The present sequence represents a cc modified hNGAL, Strep-tag II and phage coat protein pIII fragment fusion correction of the present sequence represents as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutein; human neutrophil gelatinase-associated lipocalin; hNGAL; rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin; 24p3; mutagenesis; fusion protein; cytostatic; gene therapy; tumour imaging; cancer therapy.
                                 Region
                                                                                                  Misc-difference
                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified hNGAL related fusion protein SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 400 AA;
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                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA00701 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202 WSHPQFEKQAGGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                              /note= "amber stop codon" 211. .400
                                                                                              /note= "Strep-tag II affinity tag
210
                                                                                                                                                                                                                            /note= "modified hNGAL, Strep-tag II and phage coat protein pIII fragment fusion protein" 22. .199
                                                                                                                                                                  200.
/note= "coat protein pIII fragment 217-406"
                                                                                                                                                                                                                                                                                                                                                         'label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                             note=
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85.7%;
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                                                                                                                                                                                             "mature hNGAL"
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Pred. No.
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RESULT 15 ADS20251

ADS20251 standard; protein; 646 AA

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202 WSHPQFEKQAGGGS 215

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BXH

18-NOV-2004 (first entry)

Human aggrecanase modified ADAMTS4 (mTS4) protein - SEQ ID 49.

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                                                                                                                                  Compositions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in the protein to mutagenesis at the protein. Also described: (1) a mutein of hNGAL, resulting in CC muteins of the protein. Also described: (1) a mutein of hNGAL, A2m or CC 2493 having detectable binding affinity to a given target, obtained by CC hNGAL, A2m or 2493, where an enzyme, a protein or a protein domain, a CC peptide, a signal sequence and/or an affinity tog is operably fused to CC the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the fusion protein described above, CC and a carrier. The muteins have cytostatic activity, and can be used in CC gene therapy. The method is useful in generating or producing a mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein in generating or producing a mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or the fusion protein a suspected of containing the given target under conditions that allow complex formation between the mutein and the given target and determining the complexed mutein by a suitable signal. The CC given target is a protein or protein domain, a peptide, a nucleic acid conditions that allow complex domain, a peptide, a nucleic acid cor directly for cancer therapy. The present sequence represents a cc modified hNGAL, Strep-tag II and phage coat protein pIII fragment fusion cor condition in the exemplification of the present invention.
                                               Matches
                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocalir (hNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse (24p3) uterocalin (24p3), where the mutein has a detectable affinity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or mouse 24p3/uterocalin, comprises subjecting the protein to mutagenesis.
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 96-98; 122pp; English.
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N-PSDB; ADA00732.
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16-APR-2002;
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1 WSHPQFEK--GGGS 12
                                             l Similarity
12; Conserva
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2002WO-EP004223.
                                                                   50.0%;
                                                                 Score 62; DB 6;
Pred. No. 3.8;
                                               Mismatches
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                                                                                       Length 400;
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Page 9
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Job time: 91.0813 secs
                                                                                                                    Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                     The invention relates to a novel isolated, modified ADAMTS4 (a disintegrin-like and metalloprocease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAWTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAWTS4 protein by at least one amino acid. ADAWTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The protein of the invention demonstrates osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of a human aggrecanase modified ADAMTS4 (mTS4) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; reprolysin; zinc metalloprotease; aggrecanase; osteopathic; antiinflammatory; antiiarthritic; antirheumatic; cytostatic; osteopathic; sglioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease; human; chromosome 1q21-q23; enzyme.
                                                                                                                                                                                Sequence 646 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; SEQ ID NO 49; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity for treating aggrecanase-associated conditions, including osteoarthritis.
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Freeman BA,
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(GEOR/)
(LAVA/)
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(ZENG/)
(RACI/)
(MCDO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AMHP)
                                                                                                                                                                                                             invention.
                                                           615 WLHRRAQILEILRRRPWAGRKGSAWSHPQFEK 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) RACIE L A.
) MCDONAGH T.
) FREEMAN B A.
) GEORGIADIS K E
                                                                                         μ
                                                                                                                    l Similarity
12; Conserv
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FLANNERY C R.
ZENG W.
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                                                                                      WSH-----PQFEKGGGSWSHPQFEK 20
                                                                                                                      Conservative
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Georgiadis KE,
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Lavallie ER;
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                                                                                                                                   Score 60;
Pred. No.
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                                                                                                                                                 Length 646;
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Minimum DB
Maximum DB
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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                    63.5
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*

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13: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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               US-10-026-578B-11

US-10-026-578B-3

US-10-026-578B-3

US-10-628-432-49

US-10-628-432-27

US-10-628-432-47

US-10-628-432-27

US-10-628-432-24

US-10-628-432-24

US-10-354-983-29

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US-10-358-432-25

US-10-358-283-15
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                                                                                                                                                                                                                                                                                                                                      Description
               Sequence 11, Appl
Sequence 3, Appli
Sequence 10, Appl
Sequence 40, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 8, Appli
Sequence 15, Appl
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-174-368A	-10-026-5	-10-026-5788	-10-001-934-	-10-208-357-	4-218-	US-09-813-197-8	US-09-973-145-7	09-809-51	-09-977-137A-	-09-977-137A-	-09-977-137A-	-09-977-137A-	-09-977-	-09-977-137A-	09-977-137A-	77-	7-137A-	72	US-09-983-067-3	US-09-811-284-249	US-10-425-114-53249	-425-114-44	-10-437	-10-628	-10-887-	887-228A-	-887-228A-	809-517A-3	-09-809-5	-09-809-517A-3	US-09-809-517A-30
Sequence 7, Appli	0	o N	e e	١.	"	e	7,	9	•	_	_	_	'n	Sequence 8, Appli	7,	5	e 4, Appl	6, Appl	Sequence 3, Appli	Sequence 249, App	Sequence 53249, A	4	۳.	Ç,	u	е 9	ce 1	e 34	Sequence 31, Appl	e 33	

### ALIGNMENTS

US-10-026-578B-11

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; NAME/KEY: misc feature ; OTHER INFORMATION: Artificial Sequence represents US-10-026-578B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10026578B Publication No. US20030083474A1 GENERAL INFORMATION:
APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810,010S1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR PILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 36
TYPE: PRT
Query Match
Best Local Similarity
                                                                                                                                                                              FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(28)
OTHER INFORMATION: Of the five (GGGS) repeats between position 9 and 28, one or mor:
OTHER INFORMATION: repeats may be missing. However, at least one (GGGS) repeat will
OTHER INFORMATION: be present
                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
  75.0%;
52.8%;
  Score 93;
Pred. No.
  DB 14;
2e-05;
                        Length 36;
                                                                                                     peptide binding module
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US-10-026-578B-3
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                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/10026578B Publication No. US20030083474A1 GENERAL INFORMATION:
                                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Artificial Sequence represents peptide binding
-10-026-578B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810,01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: IBA (GmbH)
APPLICANT: Schmidt,
                                                                                                                                                                                         OTHER INFORMATION: X represents a single amino
                                                                                                                                                                                                                                                          NAME/KEY: MISC_FEATURE
LOCATION: (15) . (15)
OTHER INFORMATION: X represents a single amino
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OTHER INFORMATION: X represents
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                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
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OTHER INFORMATION: X represents
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                                                                                                                                                                                                                        NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC FEATURE LOCATION: (14)..(14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: X represents a single amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: MISC FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE
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                                                                    Local
1 WSHPQFEKGGGS--
                                                      l Similarity
15; Conserv
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                                                       Conservative
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                                                                    57.3%;
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                                                    Score 71; DB 14; Length 24; Pred. No. 0.012; Indels
 WSHPQFEK 20
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US-10-026-578B-10
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TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: M101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 40, Application US/10628432
Publication No. US20040142863A1
GENERAL INFORMATION:
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SEQ ID NO 10
LENGTH: 36
                                                                      Matches
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Best Local (
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Best Local
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Publication No.
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CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
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APPLICANT: Schmidt,
                                                                                                                                                                                         LENGTH: 845
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                        FEATURE: OTHER INFORMATION: ADAMTS4 ASM with insertion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature OTHER INFORMATION: Artificial Sequence represents peptide binding module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: X represents a single amino acid at each of the positions indi OTHER INFORMATION: ed; some of the amino acids may be missing. Where amino acids OTHER INFORMATION: missing, the total numbers of x will be no less than 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: MISC_FEATURE
LOCATION: (9)..(28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                    Local Similarity
les 11; Conserv
520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WSHPQFEKGGGS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
WSHPQFEKAGG-W 531
                                WSHPQFEKGGGSW 13
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No. US20030083474A1
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                                                                    Conservative
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                                                                                    51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.4%;
                                                                    0
                                                                                    Score 63.5;
Pred. No. 3
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Pred. No. 0.11;
                                                                      Mismatches
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RESULT 5
US-10-628-432-49
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Sequence 47, Application US/10628432
Publication No. US20040142863A1
GENERAL INFORMATION:
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US-10-628-432-27
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CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27, Application US/10628432
Publication No. US20040142863A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
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Best Local Similarity
APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
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Best Local Similarity
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TITLE OF INVENTION: Modified ADAMTS4 molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 646
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: furin-processed construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 858
TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: modified ADAMTS4 molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                      827 WIHRRAQILEILRRPWAGRKGSAWSHPQFEK 858
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37.58;
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Pred. No. 7.
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Pred. No.
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Best Local Similarity
Matches 12; Conserv
Query Match
Best Local Similarity 81.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
FROM 24
                                                                                                                                                                              SOFTWARE: PatentIn Ver.
SEQ ID NO 29
LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
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Best Local Similarity
                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/354,983
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,680
PRIOR FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: AGGRECANASE MOLECULES FILE REFERENCE: 08702.0111-00000
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: AGOSTINO, MICHAEL J. APPLICANT: CORCORAN, CHRISTOPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 697
TYPE: PRT
ORGANISM: Artificial
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                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide sequence
                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               668 SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 697
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                    46.8%; Score 58; DB
81.8%; Pred. No. 0.3:
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Pred. No. 9.6;
3; Mismatches
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Pred. No. 1
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                                                    DB 15; Length 11;
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GGSWSHPQFEK 20

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US-10-358-283-15
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; Sequence 15, Applicati
; Publication No. US2000
; Publication No. US2000
; GENERAL INFORMATION:
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APPLICANT: CORCORAN, CHRISTOPHER
TITLE OF INVENTION: AGGRECANASE MOLECULES
FILE REFERENCE: 08702:0111-00000
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US/10/354,983
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: 60/353,680
PRIOR FILING DATE: 2002-01-31
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 8
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TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/10354983 Publication No. US20040044194A1 GENERAL INFORMATION:
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Best Local Similarity
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     APPLICANT: WYETH
TITLE OF INVENTION: TRUNCATED AGGRECANASE MOLECULES
FILE REFERENCE: 08702-0112-00000
FILE REFERENCE: 08702-0112-00000
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TYPE: PRT
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Construct C tag sequence
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                                                                                       Application US/10358283
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NUMBER: US/10/358,283
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Pred. No.
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FILE REFERENCE: 24745-1616
CURRENT APPLICATION NUMBER: US/10/147,211A
CURRENT FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/291,001
PRIOR FILING DATE: 2001-05-14
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 10
ORGANISM: StreptagII sequence with a one glycine linker
ORGANISM: StreptagII sequence with a one glycine linker
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US-10-147-211A-20
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                                            GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
SEQ ID NO 30
LENGTH: 21
TYPE: PRI
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PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 763
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Patent No. US20020034733A1
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Publication No. US20030235900A1
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A TRANSMEMBRANE SERINE PROTEASE 1
TITLE OF INVENTION: ENCODED POLYPEPTIDES AND METHODS BASED THEREON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Madison, Edward APPLICANT: Yeh, Jiunn-Chei
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FEATURE:
                             ORGANISM: artificial sequence
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Local Similarity 81.8%;
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Pred. No. 17;
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Page 5
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APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733Alel methods for displaying (poly) peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 33
LENGTH: 22
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
FORTURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-33
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US-09-809-517A-33
; Sequence 33, Application US/09809517A
; Patent No. US20020034733A1
; GENERAL INFORMATION:
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Search completed: March 2, 2005, 14:18:52 Job time: 63.1951 secs
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Best Local Similarity 81.8%;
Matches 9; Conservative
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Matches 9; Conserv
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                                                                                                                                                                     45.2%; Score 56; DB 9; Length 22; B1.8%; Pred. No. 1.1; ative 0; Mismatches 2; Indels
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| Maximum Match 100%
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	5002, Ap	4, Appli	25931, A	33, Appl	46, Appl	12, Appl	12, Appl	12, Appl	12643, A	6540, Ap	10, Appl	6, Appli	10283, A	4, Appli	4, Appli	4, Appli	4, Appli	THE ACTION

### ALIGNMENTS

RESULT 1 US-09-809-517A-30

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Sequence 30, Application US/09809517A

Patent No. 6753136

GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
ITILE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b
ITILE OF INVENTION: particles via disulfide bonds
ITILE OF INVENTION: particles via disulfide bonds
ITILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 30
LENGTH: 21
TYPE: PRT
Sequence 33, Application US/09809517A
Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
ITITLE OF INVENTION: No. 6753136el methods for di
ITITLE OF INVENTION: particles via disulfide bor
FILE REFERENCE: MORPHO/11
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 1999-07-20
PRIOR PILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
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Local Similarity 81.8%;
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US-09-809-517A-31
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SEQ ID NO 31
LENGTH: 24
TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity
Matches 9; Conserv
                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 34
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APPLICANT: Lohning,
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CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
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TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
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CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
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                                                                                                          PRIOR APPLICATION NUMBER: EP 99114072.4 PRIOR FILING DATE: 1999-07-20 PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR FILING DATE: 2000-02-18
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TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
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OTHER INFORMATION: Description of Artificial Sequence: synthetic module
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ORGANISM: artificial sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-809-517A-34
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US-09-977-137A-4
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US-09-809-517A-6
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                                                     US-09-977-137A-4
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Best Local
                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09977137A Patent No. 6750042
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Matches 8; Conserv
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Query Match
Best Local Similarity
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                                                                                                                                                                                                           APPLICANT: Caggiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
FRIOR APPLICATION NUMBER: US 60/240,465
REIOR EILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on TITLE OF INVENTION: particles via disulfide bonds FILE REFERENCE: MORPHO/11 CURRENT APPLICATION NUMBER: US/09/809,517A CURRENT FILING DATE: 2001-03-15 CURRENT FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR FILING DATE: 2000-02-18 NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: EP 99114072.4 PRIOR FILING DATE: 1999-07-20
                                                                                                                                                                                      PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Summers, APPLICANT: Caguiat,
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ORGANISM: artificial sequence
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                                                                      FEATURE:
OTHER INFORMATION:
                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                         TYPE: PRT
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                                                                                                                                          ENGTH: 117
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es 9; Conserv
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                                                                    Description of Artificial Sequence: chelon
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Pred. No. 0.13;
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Pred. No. 0.
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RESULT 7
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US-09-977-137A-7
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Best Local Similarity 88.
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
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                                                            Query Match
Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 5
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
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                                                                                                                                                   TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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109 AWSHPOPEK 117
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Pred. No. 2
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US-09-977-137A-9
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Patent No. 6750042
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
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Matches
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 9
LENGTH: 117
TYPE: PRT
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
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ORGANISM: Artificial Sequence
FEATURE:
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nes 8; Conserv
109 AWSHPQFEK 117
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Pred. No. 2
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Pred. No. 2.7;
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RESULT 11 US-09-977-137A-10

Sequence 10, Application US/09977137A Patent No. 6750042 GENERAL INFORMATION:

APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonathan

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US-09-977-137A-12
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; APPLICANT: Summers, Anne O.; APPLICANT: Cagulat, Jonathan; TITLE OF INVENTION: Metal Binding Proteins, Re; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                               Sequence 12, Application US/09977137A Patent No. 6750042
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SEQ ID NO 11
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 10
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
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TYPE: PRT
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Pred. No.
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Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.0
SEO ID NO 6
SENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                         SEQ ID NO 2
LENGTH: 8
                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08948097C Patent No. 6103493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Patent No. 6750042
GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                        FILE REFERENCE: HUBR 1119
CURRENT APPLICATION NUMBER: US/08/948,097C
CURRENT FILING DATE: 1997-10-09
EARLIER APPLICATION NUMBER: DE 196 41 876.3
EARLIER FILING DATE: 1996-10-10
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                            APPLICANT: Skerra, Arne
APPLICANT: Voss, Selma
TITLE OF INVENTION: Streptavidin Muteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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NAME/KEY: BINDING
OTHER INFORMATION: Binding ligand for streptavidin
                                      FEATURE:
                                                      ORGANISM: Artificial sequence
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1; Mismatches
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Pred. No. 2.
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Perfect score:
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Listing first 45 summaries
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 GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
AB2153
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33.9	34.2	34.2	34.2	34.2	34.2	34.2	34.2	34.2	34.2	34.2	34.6	34.6	34.6	34.6	34.9
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T24470	G87398	A38447	T01013	F86341	S68798	T21222	A23544	853631	F90197	XMBSTA	QQBE9	A54281	S37149	JU0268	B42239
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p  ay-1995 #text_change 09-Jul-2004  gene expression in stratified squamous epith pMID:7909356  pMID:9508989; PIDN:AAA59965.1; PID:g508990 t-51 is the initiator pMID:8451175	0.83; ches 4	(strain PCC 7120)  onym of Anabaena sp. strain PCC 7120 ec-2001 #text_change 09-Jul-2004 itz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi kazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S ilamentous Nitrogen-fixing Cyanobacterium Ana pMID:11759840  0019; PIDN:BAB74476.1; PID:gl7131870; GSPDB:C	NTS	hypothetical prote major prion protei major prion protei protei hypothetical protei hypothetical protei hypothetical protei hypothetical protei hypothetical protei hypothetical protei hypothetical proteinisopeptide ABC tacrB/AcrB/AcrF fam hypothetical protein

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A;Cross-references: EMBL:X54628; NID:g53505; PIDN:CAA38445.1; PID:g53506 R,Suzuki, N.; Rohdewohld, H.; Neuman, T.; Gruss, P.; Schoeler, H.R. EMBO J. 9, 3723-3732, 1990
A;Tile: Oct-6: a POU transcription factor expressed in embryonal stem ce A;Reference number: S11999; MUID:91006074; PMID:1976514
A;Accession: S11999
A;Molecule type: mRNA
A;Residues: 1-26,28-449 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                            transcription factor Oct-6 - mouse

N;Alternate names: class III POU domain protein SCIP
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S30205; S31226; S13083; S11999
R;Zimmerman, E.C., Jones, C.M.; Fet, V.; Hogan, B.L.M.; Magnuson, M.A.
Nucleic Acids Res, 19, 956, 1991
A;Title: Nucleotide sequence of mouse SCIP cDNA, a POU-domain transcription
A;Reference number: S30205; MUDI:91204458; PMID:1840678
A;Accession: S30205
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 51-448 <TOB>
A;Cross-references: EMBL:Z18284; NID:g35133; PIDN:CAA79158.1; PID:g35134
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: transcription factor Brn-1; homeobox homology; POU down C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;251-318,Domain: POU domain homology <POU>F;337-393/Domain: homeobox homology <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:D21952; EMBL:X56959; NID:g49681; PIDN:CAA40280.1; A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Decemb R;Hara, Y.; Rovescalli, A.C.; Kim, Y.; Nirenberg, M. Proc. Natl. Acad. Sci. U.S.A. 89, 3280-3284, 1992 A;Title: Structure and evolution of four POU domain genes expressed in mouse b A;Reference number: S31223; MUID:92228768; PMID:1565620 A;Accession: S31226
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                                                                                            C;Superfamily: transcription factor
C;Keywords: DNA binding; homeobox; r
F;252-319/Domain: POU domain homolog
F;338-394/Domain: homeobox homology
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                                                                                                                   A;Cross-references: EMBL:X57482; NID:g53507; PIDN:CAA40720.1; PID:g53508
C;Superfamily: transcription factor Brn-1; homeobox homology; POU domain homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;252-319/Domain: POU domain homology <POU>
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A;Residues: 1-449 <HAR>
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A; Residues: 1-449 <ZIM>
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Best Local S
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3; Mismatches
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                                                                     ABC protein AGR I 3000 (AB015053) [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                                     RESULT
D98318
                       C;Accession: D98318
R;Goodner, B.; Hink
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RESULT 4
A40168
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A; Residues: 265-319,'A',321-335;336-389 <HEF>
A; Residues: 265-319,'A', 321-335;336-389 <HEF>
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A;Title: Tst-1, a member of the POU domain gene family, binds the promoter of the gene & R;Reference number: A39694; MUID:91141528; PMID:1705013
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A;Title: Expression and activity of the POU transcription factor SCIP
A;Reference number: A40168; MUID:90378306; PMID:1975954
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A;Residues: 265-389 <HEX>
A;Residues: 265-389 <HEX>
A;Rote: this is a revision to the sequence from reference S05042
A;Note: this is a revision to the sequence from reference S05042
A;Note: this is a revision to the sequence from reference S05042
Nature 340, 35-42, 1989
A;Title: Expression of a large family of POU-domain regulatory genes
A;Reference number: S05042; MUID:89295573; PMID:2739723
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A;Residues: 35-451 <HBA>
A;Residues: 35-451 <HBA>
A;Cross-references: GB:M63712; NID:g207539; PIDN:AAA42303.1; PII
A;Cross-references: GB:M63712; NID:g207539; PIDN:AAA42303.1; PII
A;Cross-references: GB:M63712; NID:g207539; PIDN:AAA42303.1; PII
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A;Title: Correction. Expres
A;Reference number: S05449
A;Accession: S05449
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Hinkle,

G.;

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Miller, N.; Blanchard, M.; Qurollo, Doughty, D.; Scott, C.; Lappas, C.;

B.; Goldman, Markelz, B.,

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RESULT 6
F84946
                                                                                                                                                                               R;Waite, J.H.; Jensen, R.A.; Morse, D.E. Biochemistry 31, 5733-5738, 1992
A;Title: Cement procursor proteins of the : A;Reference number: A42627; MUID:92304953; A;Accession: B42627
                                                                                                                                                                                                                                                              cement precursor protein Pc-2 - polychaete (Phragmatopoma californica) (fragments) C;Specias: Phragmatopoma californica C;Date: 03.Feb-1994 #sequence_revision 03.Feb-1994 #text_change 09-Jul-2004 C;Accession: B42627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: D98318
á
                                                                                             A;Cross-references: UNIPROT:Q7M3Q2
C;Comment: This protein becomes a component of the quinone-tanned cement in the tubes bu F;30,32,53,56,76,89,92,105,108,129,136,149/Modified site: 3',4'-dihydroxyphenylalanine (
                                                                                                                                               A; Molecule type: protein A; Residues: 1-161 < WAI>
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A; Residues: 1-1079 <STO>
A; Cross-references: GB:AP000398; GSPDB:GN00144
A; Experimental source: strain APS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision
C;Accession: F84946
R;Shigenobu, S:; Watanabe, H.; Hattori,
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                               Matches
                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                            Length 161;
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C;Accession: T20863
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Matches 12
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les 12; Conserv
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 317
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 WTIPQWEKQLYDAVSEMEGGETGDDSWSFDKF 348
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A; Mistatus, France, A; Mistatus, France, DNA
A; Molecule type: DNA
A; Residues: 1-621 <WIL>
A; Cross-references: EMBL: Z68748; PIDN: CAA92953.1; GSPDB: GN00022; CESP: F13H10.3
A; Cross-imental source; clone F13H10
                                                                                                                                                                                                                                                                                                                                                                                  R;Cottage, A.
submitted to the EMBL Data Library,
a.Paference number: Z19335
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A;Introns: 9/3; 255/1
A;Introns: 9/3; 255/1
C;Superfamily: helix-destabilizing protein; ribonucleoprotein
C;Superfamily: ribonucleoprotein repeat homology <RRM1>
F;24-90/Domain: ribonucleoprotein repeat homology <RRM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Du, Z.; Scheet, P.; Andrews, S. submitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid | A;Reference number: Z21201 A;Accession: T32620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Iwasaki, M.; Okumura, K.; Kondo, Y.; Tanaka, T.; Igarashi, H. Nucleic Acids Res. 20, 4001-4007, 1992
A;Title: cDNA cloning of a novel heterogeneous nuclear ribonucleoprotein gene A;Reference number: S35500; MUID:92375884; PMID:1354852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heterogeneous ribonuclear particle protein homolog - Caenorhabditis N;Alternate names: heterogeneous nuclear ribonucleoprotein homolog C;Species: Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Experimental source: strain Bristol N2; clone F42A6 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-346 <DUZ>
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A;Residues: 1-346 <IWA>
A;Cross-references: UNIPROT:Q22037; EMBL:S43152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:AF038613; PIDN:AAB92051.1; GSPDB:GN00022; CESP:F42A6.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F13H10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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WSHPQFEK-----
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- GGGSGGGSWSHPQF 22
                                                Score 56; DB Pred. No. 20; 4; Mismatches
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A,Description: required for activated transcription; binds RNA & C,Superfamily: RNA-binding protein, EWS type; ribonucleoprotein C,Keywords: RNA binding
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A,Title: hTAFII68, a novel RNA/ssDNA-binding protein with A,Reference number: S71954; MUID:97045110; PMID:8890175
A,Accession: S71954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA/8sDNA-binding protein TAFII68 - human
N;Alternate names: TATA-binding protein-associated factor TAFII68
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P19622
R;Poole, S.J.; Law, M.L.; Kao, F.T.; Lau, Y.F.
Genomics 4, 225-231, 1989
A;Title: Isolation and chromosomal localization of the human En-2
A;Reference number: A30141; MUID:89233109; PMID:2565873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 16-Aug-2004
C;Accession: E48423; A30141
R;Logan, C.; Hanks, M.C.; Noble-Topham, S.; Nallainathan, D.; Provart, N.J.
Dev. Genet. 13, 345-358, 1992
Dev. Genet. 13, 345-358, 1992
A;Title: Cloning and sequence comparison of the mouse, human, and chicken e A;Reference number: A48423; MUID:93185339; PMID:1363401
A;Accession: E48423
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R; Bertolotti, A.; Li
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                                                                                                                                                                                                                                                        A;Accession: A30141
A;Molecule type: DNA
A;Residues: 230-333 <POO>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: taf68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q92804; EMBL:X98893; NID:g1628402; PIDN:CAA67398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-589 <BER>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          omeotic protein engrailed 2 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Homo sapiens (man)
,Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Function:
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Best Local
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                                                                                                     Query Match
Best Local
                                                                                                                                                                      245-301/Domain: homeobox homology
                                                                                                                                                                                       Superfamily: homeobox homology Keywords: DNA binding; homeobox; nucleus;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues: 1-333 <LOG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Status: preliminary; not compared with conceptual translation
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9; Conserv
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    PESSPGGGGGGGGSSP
                                          POFEKGGGSGGSWSHP 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.7%;
                                                                                                        37.0%;
    37
                                                                                    Score 54; DB Pred. No. 19; 1; Mismatches
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Pred. No.
                                                                                                                                                                        <XOX>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S.; Nallainathan, D.; Provart, N.J.; Joyner,
                                                                                                 DB
19;
                                                                                                                                                                                   transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                              Length 333;
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1-phosphatidylinositol 3-kinase (EC 2.7.1.137) - N/Alternate names: phosphatidylinositol 3-kinase (Species: Chlamydomonas reinhardtii C/Date: 11-Jun-1999 #sequence_revision 11-Jun-199 C/Accession: T08420
R/Molendijk, A.J./ Irrine, R.F.
                                                                                                                                  RESULT 14
T08420
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RESULT 13
G71521
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A;Title: Genome sequences of Chlamydia trachomatis MoPn and A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: F81678
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                                                                                                                                                                                                                                                                                                                                                                                                                   R;Stephens, R.S.; Kalman, Science 282, 754-759, 1998
A;Title: Genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable GTP binding protein - Chlamydia trachomatis (serotype D, strain UW3)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
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A;Experimental source: serotype D, strain UW-3/Cx
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A; Residues: 1-447 < TET>
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                                                                                                                                                Superfamily: GTP-binding protein hflX; translation elongation; Reywords: nucleotide binding; P-loop; 233-240/Region: nucleotide-binding motif A (P-loop); 346-349/Region: GTP-binding NKXD motif; 371-373/Region: GTP-binding SAK/L motif
                                                                                          Query Match
Best Local
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165
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WCHLSROKSGGSGGG
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                                                                            Conservative
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179
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                                                                            Mismatches
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G.; Salzberg,
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11-Jun-1999

#text\_change

Chlamydomonas

reinhardtii (fragment)

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unknown protein F14G9.26 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96G03
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Lil, J.H.; Li, Y.; Liu, S.X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                   Query Match
Best Local Similarity
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Search completed: March Job time: 19.3415 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:004269; EMBL:U97662; NID:g2109288; PIDN:AAC50017.1; PID:g210A;Experimental source: strain cw-15
C;Function:
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A;Accession: T08420
                                                                                                                                                                                                                                                                                                                       A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-154 <STO>
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A; Residues: 1-732 < MOL>
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Pred. No. 16;
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Maximum Match 100%
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Tettelin H., Nelson K.E., M., Brinkac L.M., Daugher

Daugherty S.C.,

NCBI\_TaxID=243160;

062N21 PRELIMINARY; PRT; 429 AA.
062N21;
25-CCT-2004 (TrEMBLrel. 28, Created)
25-CCT-2004 (TrEMBLrel. 28, Last sequence update)
25-CCT-2004 (TrEMBLrel. 28, Last annotation update)
Capsular polysaccharide biosynthesis/export periplasmic protein.
ORFNames=BMA0047;

Burkholderia mallei ATCC 23344. Bacteria, Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia.

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Q1-MAR-2003 (TrEMBLrel. 23, Created)
Q1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Guanyly1 cyclase alpha 1 subunit.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Ratkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Marinae; Ratt
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Bentley S.D., Sebalhia M., Thomson N.R., Bason N., Beacham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels I.
Keith K.E., Maddison M., Moule S., Price C., Quall M.A.,
Kabhinowitsch E., Rutherford K., Sanders M., Simmonds M.,
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
Songsivilai S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.,
"Genomic plasticity of the causative agent of melioidosis,
Grand T., Burkholderia near-domailet ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Burkholderia pseudomallei.";
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
EMBL; BX571965; CAH34612.1; -
SEQUENCE 429 AA; 45877 MW; 7A4129C970AECC98 CRC6
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Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
Atkins T., Crossman i.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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ORFNames=BPSL0619;
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EMBL; CP000010; AAU48949.1; -.
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45905 MW; 614129D67FBED397 CRC64;
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biosynthesis/export protein.
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                                                           Q9WX37;
Q9WX37;
01-NOV-1999
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05-JUL-2004
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SEQUENCE
01-MAR-2004 (TrEMBLrel. 26, Last anno
RNA binding protein.
Name=rbpE; OrderedLocusNames=all2777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000504; RNA rec_mot.
Pfam; PF00076; RRM 1; 1.
SMART; SM00360; RRM; 1.
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HSSP; P30803; IAZS.
GO; GO:0004383; F:guanylate cyclase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade;
                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50102; RRM; 1.

PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.

SEQUENCE 99 AA; 10811 MW; 893B196FC8187798 CRC64;
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PROSITE; PS00452; GUANYLATE C
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Bacteria; Cyanobacteria;
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Submitted (NOV-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=rbpE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [nterPro; IPR001054; G_cyclase.
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16; Conserv
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                                                                                                                                                                                                                                                                          SHPQFEKGGGSGGGSWS
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                                                           (TrEMBLrel.
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64.7%;
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Last sequence update)
Last annotation update)
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Pred. No. 5.1;
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A Nakamura I., Yao Y., Suzuki N.;
A Nakamura I., Yao Y., Suzuki N.;
A Nakamura I., Yao Y., Suzuki N.;
A Nakamura I., Yao Y., Suzuki N.;
A Nakamura I., Yao Y., Suzuki N.;
EMBL; AB097860; BAC44887.1; -
DR GG; G0:0004383; F:guanylate cyclase activity; IEA.
DR GO; G0:000742; F:lyase activity; IEA.
DR GO; G0:000742; F:lyase activity; IEA.
DR GO; G0:000742; P:intracellular signaling cascade; IEA.
DR InterPro; IPR001054; G_cyclase.
DR InterPro; IPR001054; G_cyclase.
DR InterPro; IPR001054; G_cyclase.
DR Ffam; PF00211; Guanylate_cyc; 1.
DR SMART; SM00044; CYCG; 1.
DR PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.
DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
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Matches 10
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MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,

Yasuda M., Tabata S.;

"Complete genomic sequence of the filamentous nitrogen-fixing

"Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00076; RRM_1; 1.
SMART; SM00360; RRM; 1.
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PS00030; RRM_RNP_1;
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99 AA; 10811 MW;
GSWSHPOFEK 743
                                                   GSWSHPQFEK 24
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Pred. No.
                                                                                                                                   Score 61;
Pred. No.
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1 003052;

2 003052;

2 01-JUL-1993 (Rel. 26, Created)

T 01-CCT-1996 (Rel. 34, Last sequence update)

T 01-CCT-1996 (Rel. 44, Last annotation update)

DE POU domain, class 3, transcription factor 1 (October 1)

Post Companion factor 6) (Oct-6) (POU-domain transcription factor 6)
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Matches 9
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A Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
A Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
A Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
A Hijishita S., Honda M., Ichikawa Y., Icoh Y., Iishikawa M., Kamiya K.,
A Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
A Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
A Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
A Karasawa W., Machara T., Mizuno H., Mizubayashi T., Mukai Y.,
A Nagasaki H., Nakashima M., Nakama Y., Nakamini Y., Nakamura M.,
A Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
A Namiki N., Vamagata H., Song J., Takazaki Y., Terasawa K., Tsuji K.,
A Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
A Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
A Maki K., Yamagata H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
Yano M., Jiang J., Gojobori T.,
The Genome Semence and structure of rice chromosome 1 ""
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Q9LGE7;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 28, Last sequence
25-CCT-2004 (TrEMBLrel. 28, Last annotati
P0406H10.1 protein (P0509B06.3 protein).
Name=P0406H10.1; Synonyms=P0509B06.3;
Name=P0406H10.1; Synonyms=P0509B06.3;
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InterPro; IPR002794; DUF92.
Pfam; PF01940; DUF92; 1.
ProDom; PD014594; DUF92; 1.
SEQUENCE 929 AA; 100025 MW;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
Faus I., Hsu H.J., Fuchs E.,
"Oct-6: a regulator of keratinocyte
squamous epithelia.";
Mol. Cell. Biol. 14:3263-3275(1994).
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                Name=POU3F1; Synonyms=OCT6,
Homo sapiens (Human).
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PubMed=12447438; D
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                                                                                                                         MEDLINE=94217723; PubMed=7909356;
                                                                                                                                                             SEQUENCE FROM
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Similarity 52.9%;
9; Conservative
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Pred. No.
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01-OCT-2002
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SEQUENCE OF 51-448 FROM N.A.
MEDLINE-93197134; PubMed-8451175;
MEDLINE-93197134; PubMed-8451175;
MEDLINE-93197134; PubMed-8451175;
MEDLINE-93197134; PubMed-8451175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 602479; -.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0008366; P:nerve ensheathment; TAS.
InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain like.
InterPro; IPR009057; Homeodomain like_DNA.
InterPro; IPR0090327; POU.
InterPro; IPR007103; POU.
InterPro; IPR007103; POU.
InterPro; IPR007103; POU.
InterPro; IPR007103; POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L26494; AAA59965.1; -. EMBL; Z18284; CAA79158.1; -. PIR; A56018; A56018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                 ProDom; PD000010; Homeobox; 1.
ProDom; PD000583; POU; 1.
PROSITE; PS00027; HOMEOBOX 2; 1.
PROSITE; PS00035; POU 1; 1.
PROSITE; PS00035; POU 2; 1.
PROSITE; PS00465; POU 2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00046; Homeobox; 1.
Pfam; PF00157; Pou; 1.
PRINTS; PR00024; HOMEOBOX.
PRINTS; PR00028; POUDOMAIN.
                  CG5913-PA.
ORFNames=CG5913;
                                                                                                                                                                                                                                                                                                                        DNA-binding; Homeobox; Nuclear protein; DOMAIN 248 318 POU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC; T00655; -.
Genew; HGNC:9214; POU3F1.
    Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and neurogenesis.
SUBCELLULAR LOCATION: Nuclear.
TISSUE SPECIFICITY: Expressed in embryonal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 subfamily.
SIMILARITY: Contains 1 homeobox domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leic Acids Res. 21:1043-1043(1993). FUNCTION: Transcription factor tha
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SIMILARITY: Belongs
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                                                                                                                                                                                                        2 SHPQFEKGGGSGGSWSHPQFE
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Oct-6 POU transcription factor lacks
ts murine counterpart.";
                                             (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                              448 AA;
                                                                                                                                                                                                                                     Conservative
                                                                                                        PRELIMINARY;
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395
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                                                                                                                                                                                                                                                                                              45270 MW;
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                                                                                                                                                                                                                                                                                                            Homeobox
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Pred. No.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., RA Mann K.H., Doyle C., Barter B.G., Champe M., Ffeiffer B.D., RA Barliw R.M., Dayle C., Barter B.G., Helt G., Nelson C.R., Gabor G.L., Raber B.C., Rogers Y.H., Blazej R.G., Champe M., Ffeiffer B.D., RA Barliw R.M., Dayle C., Barter B.G., Helt G., Nelson C.R., Gabor G.L., RA Barliw R.M., Dayle C., Barter B.G., Helt G., Nelson C.R., Gabor G.L., Ra Barliw R.M., Dayle A., An H.J., Andrews-Pfannkoch C., Baldwin D. Balliw R.M., Bauel A., Baxendale J., Barshararglu L., Beasley E.M., Balliw R.M., Bouck J., Brokstein P., Botther P., Ra Bartis K.C., Busen D.A., Butler H., Cadieu E., Center A., Chandra I., Erchry J.M., Cawley S., Dahlke C., Davenport L.B., Davise P., Ra Borkova D., Botthar M.R., Bouck J., Brokstein P., Brottler P., Ra Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Charlis M.L., Harvey D., Helman T.J., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Werimer J., Houck J., Ra Harris N.L., Harvey D., Helman T.J., Werimison J.A., Ketchum K.A., Ra Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Ra Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Nount S.M., Moy M., Murphy B., Murphy L., Murpy D.M., Nelson D.L., Ra Keinert K., Remington K., Saunders R.D., Scheeler F., Shen H., Ra Adams C., Strabler R.D., Scheeler F., Shen H., Shue B.C., Sten S.M., Woodaget, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J., Ra Spier E., Zhan M., Zhang G., Zhao Q., Zhao Q., Ye J., Rhi S., Zhu X., Smith H.O., Spience S. Shue B.C., Staplence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=2246065; PubMed=12537568;

MEDLINE=2246065, Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Celniker S.E., Wheeler D.A., Kronmiller B., Frise E., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Berman B.P
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P
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Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                      Ashburner M., Celniker S.E.;
"The transposable elements of the a genomics perspective.";
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MEDLINE=22426070; PubMed=12537573;
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                                                                                                                                                                                                                                                                                                 Kronmiller
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                                         Berman B.P.,
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RESULT 12
Q7QG12
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O1-MAR-2004 (TrEMBLrel. 26, Last annotation upd
DE AGCP13661 (Fragment).
Name=agCG51770; ORFNames=ENSANGG00000012651;
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Submitted (MAR-2004) to the
EMBL; AE003754; AAF56525.1;
IntAct; O9VBK9; -
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STADDICTOR M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Conzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AY052130, AAK93554.1; -.

FlyBase, FBgn0039385; CG5913.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Eddopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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454 AA; 49967 MW;
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.

Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,

Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt

Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,

Yang Q.O., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,

White O., Salzberg S.L., Fraser C.M.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplanteae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AAABO1008844; EAAO5947.1; -.
InterPro; IPR009818; Ataxin-2 C.
InterPro; IPR009604; Ataxin-2 N.
InterPro; IPR01920; Sm like_riboprot.
Pfam; PF06741; Ataxin-2 N; 1.
Pfam; PF07145; PAM2; 1.
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Ano
NCBI_TaxID=180454;
[1]
                                                                                                                                                                                  Hypothetical protein. SEQUENCE 82 AA; 9050 MW;
                                                                                                                                                                                                                                                    Buell R.;
Submitted (JAN-2004)
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Name=OSJNBb0106M04.14;
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RESULT 14 Q7X243 ID Q7X24 AC Q7X24

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"Production of Cellulose and Curli Fimbriae by
Enterobacteriaceae Isolated from the Human Gas'
Infect. Immun. 72:4151-4158(2003).
EMBL; AJ515700; CAD56672.1; -.
GO; GO:0009289; C:fimbria; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
FEam; PF07012; Curlin_rpt.
SEQUENCE 150 AA; 15016 MW; 1D7141B8D6973DC
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01-MAR-2004 (TrEMBLre
Curlin-cegA protein.
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Enterobacteriaceae; Citrol
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01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation factor 1 (Octamer-binding
POU domain, class 3, transcription factor 1 (Octamer-binding
transcription factor 6) (Oct-6) (POU-domain transcription factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6 X CBA; TISSUB-Brain;
MEDLINE=91081324; PubMed=1979677;
Meijer D., Graus A., Kraay R., Langeveld A., Mulder M.P., Grosveld G.;
"The octamer binding factor Oct6: cDNA cloning and expression in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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                                                                                                                                     MEDLINE=91204458; PubMed=1840678; Zimmerman E.C., Jones C.M., Fet V., "Nucleotide sequence of mouse SCIP"
       SEQUENCE FROM N.A.
MEDLINE=92228768; PubMed=1565620;
Hara Y., Rovescalli C., Kim Y., N
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                                                                                                Acids Res.
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Citrobacter.
                                                                                                     19:956-956(1991).
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; Murinae; Mus.
                                                                                                                                                           transcription
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EMBL; X56959; CAA40280.1; -.
EMBL; X56959; CAA40720.1; -.
EMBL; X57482; CAA40720.1; -.
EMBL; M88302; AAA39963.1; -.
EMBL; S30205; S30205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PRINTS;
ProDom;
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InterPro; IPR001356; Homeobox.
InterPro; IPR009057; Homeodomain like.
InterPro; IPR019982; Lambda_like_DNA.
InterPro; IPR010327; POU.
InterPro; IPR017103; POU homeo.
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CONFLICT
SEQUENCE
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GO; GO:0005634; C:nucleu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 subfamily.
SIMILARITY: Contains 1 homeobox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 89:3280-32 FUNCTION: Transcription factor that (5'-ATTTGCAT-3'). Thought to be involuded in the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second o
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SIMILARITY: Belongs to the POU transcription
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PR00028; POUDOMAIN.
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52.9%;
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                                                                                                                                                                                                       Score 58;
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Missing (in Ref. 2).
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m ir} protein; Transcription regulation poU.
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein -

protein search, using sw model

Title: Perfect score: Run on: SEQ11 March 2, 2005, 12:20:44 ; Search time 108.098 Seconds (without alignments) 85.869 Million cell updates/sec

Scoring table: Sequence: Gapop 10.0 , BLOSUM62DX 1 wshpqfekgggsgggswshpqfek 24 Gapext 0.5

Total number of hits satisfying chosen parameters: 2105692

2105692 segs, 386760381 residues

Searched:

Post-processing: Minimum Match 0%
'Maximum Match 100%
'Listing first 45 summaries Minimum DB Maximum DB seq length: 0 seq length: 2000000000

A Geneseq\_16Dec04:\*
1: geneseqp1980s:\*
2: geneseqp1990s:\*
3: geneseqp2000s:\*
4: geneseqp2001s:\*
5: geneseqp2003s:\*
6: geneseqp2003s:\*
7: geneseqp2003bs:\*
8: geneseqp2004s:\*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	o	Ç,	4	ω	N	<b>-</b>	Result
59	59	60	61	61	63	63	63	63	63.5	66	69	69.5	71.5	71.5	75	84	84	84	84	84	84	84	84	130	Score
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45	44	<b>4</b> 3	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
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ADA00709	AAY92150	ADN11226	ADN11207	ADN11225	ADN11208	ADI39156	ADI39155	ABG74880	ABG74881	ADS20228	AAE38373	ADO19053	AD019051	AAU97554	AAU97560	AAU97552	AAU97556	AAU97555	AAU9/55/
Ada00709	Aay92150	Adn11226	Adn11207	Adn11225	Adn11208	Adi39156	Adi39155	Abg74880	Abg74881	Ads20228	Aae38373	Ado19053	Ado19051	Aau97554	Aau97560	Aau97552	Aau97556	Aau97555	/ cc/ knew
Modified	C19-jun f		Peptide m	Peptide m	Peptide m	Construct	Construct	Bacteriop	Bacteriop	Strep tag	Epitope t	Murine an	Murine an	Synthetic	Synthetic	Synthetic	Synthetic	Synthetic	synthetic

# ALIGNMENTS

RESULT 1

ABP60370	0370
ij	ABP60370 standard; peptide; 36 AA.
A X	ABP60370;
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ij	28-MAR-2003 (first entry)
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E	Streptavidin binding peptide SEQ ID NO 11.
×	
₹	Streptavidin; protein chip; microtitre plate; detection.
Š	
လ္ထ	Synthetic.
×	
Ŧ	Key Location/Qualifiers
Ŧ	ion
FT	<pre>/note= "GGGS repeats 2-5 optionally absent, residues 13-</pre>
ΡŢ	28"
Ŧ	Region 912
Ŧ	
×	
PN	DE10113776-A1.
×	
B	02-OCT-2002.

02-0CT-2002.

21-MAR-2001; 2001DE-01013776.

21-MAR-2001; 2001DE-01013776.

(BIOA-) INST BIOANALYTIK GMBH GOETTINGEN.

Schmidt T;

WPI; 2003-031166/03.

New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding modules.

Claim 8; Page 16; 18pp; German.

The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides

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                                                                                 WPI; 1999-255093/21.
N-PSDB; AAX24099.
                                 Disclosure; Page 67-69;
                                                   New anticalins produced by mutation of lipocalin family protein
                                                                                                                                                              26-SEP-1997;
                                                                                                                                                                                     25-SEP-1998;
                                                                                                                                                                                                             08-APR-1999.
                                                                                                                                         (SKER/) SKERRA
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                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pBBP20 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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22. .1
                                                                                                                                                                                                                                                                                                                                              /label= fusion_peptide
/note= "This fusion peptide is constructed from bilin
binding protein, a strep-Tag II region and a fragment
phage coat protein pIII"
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207. .396
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                                                                                                                  Schmidt
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This invention describes the preparation of anticalins from polypeptides of the lipocalin family by mutation of amino acids in the region of the

80pp; German.

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RESULT 3
AAB46420
ID AAB4
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   This invention describes novel polypeptides (I) that are muteins of bilin binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being simpler structure and are easier to prepare. They have a specificity for Dig, relative to other steroids, and fusion partners may be attached to either end without compromising their ability to bind 11-a-n
                                                                                                                                                                                                                                                                                                   New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide loops (at one end of the cylindrical 'leaflet' structure). Anticalins can bind to a predetermined ligand with determinable affinity. Anticalins or fusions of anticalins, are used: (a) when immobilized, for separation; and (b) when labeled, for identification of ligands (or their fusions or conjugates). Typically they bind to tissue- or tumor-specific surface molecules and can be used for tumour imaging or directly for tumour therapy. Mutations can be introduced into lipocalin polypeptides more easily than into antibodies, since lipocalin polypeptides have only (contrast 6) sequence segments. The peptide loops can tolerate amino acid changes without significant effect on folding. Anticalins have high specific affinity, comparable with that for antibodies. This sequence represents a fusion polypeptide used in the method of the invention
                                                                                                                                                                                                                                                     Example 1; Page 55-56; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bilin binding-protein associated protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;666T-NOL-80
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                                                                                                                                 have an amino acid (aa) substitution at at least one of the positions 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 1125 or 127. (I), or i fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being used as a label. Compared with Dig-specific antibodies, (I) have a simpler structure and are easier to prepare. They have very high specificity for Dig, relative to other steroids, and fusion partners m be attached to either end without compromising their ability to bind
                                                                                                                                                                                                                                                              This invention describes novel polypeptides (I) that are muteins of bilin-binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and
                                                                                                                                                                                                                                                                                                                                                      New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
                                                                                                                                                                                                                                                                                                                                                                                                                                  Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bilin-binding protein; mutein; BBP; digoxigenin
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                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                            The present invention relates to a method for generating muteins of human neutrophil gelatinase-associated lipocalin (NNGAL), rat alpha2-microglobulin-related protein (A2m) or mouse 24p3/uterocalin, by subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the coat protein pIII of a filamentous bacteriophage of the M13-family of a fragment of the coat protein. The present sequence is the protein encoded by a fragment of plasmid pHNGAL5, used to illustrate the invention. This sequence comprises human hNGAL, a Strep-Tag II and a fragment of phage coat protein pIII.
                                                                                                                                                                                                                                                                                                                       Generating a mutein of a protein for validating the protein as drug target by subjecting the protein to mutagenesis at sequence positions corresponding to sequence positions of the human neutrophil gelatinase-associated lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutein; human; neutrophil gelatinase-associated lipocalin; hNGAL; rat; alpha2-microglobulin-related protein; A2m; mouse; 24p3; uterocalin.
                                                                                                      Sequence 400
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                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-381639/36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "Amino acids 217-406 of coat protein pIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "Encoded
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coat protein pIII"
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                                                                                                                       The present invention relates to a method for generating muteins of human neutrophil gelatinase-associated lipocalin (hNGAL), rat alpha2-microglobulin-related protein (A2m) or mouse 24p3/uterocalin, by subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the coat protein piII of a filamentous bacteriophage of the M13-family or for a fragment of the coat protein. The present sequence is the protein encoded by a fragment of plasmid pHNGAL3, used to illustrate the invention. This sequence comprises human hNGAL, a Strep-Tag II and a
                                                                                           Sequence 400 AA;
                                                                                                                                                                                                                                                                                                Generating a mutein of a protein for validating the protein as drug target by subjecting the protein to mutagenesis at sequence positions corresponding to sequence positions of the human neutrophil gelatinase-associated lipocalin.
                                                                                                                                                                                                                                                                       Disclosure; Page 59-61; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADA27286
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Tag II and a fragment of phage coat protein pIII"
22. .199
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                16
                                    Score 84; DB of Pred. No. 0.090 Pred. No. 0.090
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given target, comprising subjecting the protein to mutagenesis at positions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in mutains of the protein. Also described: (1) a mutain of hNGAL, A2m or 2493 having detectable binding affinity to a given target, obtained by the method described above; (2) a fusion protein comprising the mutein of hNGAL, A2m or 2493, where an enzyme, a protein or a protein domain, a peptide, a signal sequence and/or an affinity tag is operably fused to the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the fusion protein of (2); and (4) a pharmaceutical composition comprising
                                                                                                                                                                                                                                                                             The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocalir (hNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse 24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or m 24p3/uterocalin, comprises subjecting the protein to mutagenesis.
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16-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 94-95; 122pp; English.
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DB; ADA00731.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIERIS PROTEOLAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    imaging;
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protein pIII fragment fusion protein"
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                                                                                                                                                                                                                                                                                                                                     mutein or a iated lipocalin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour imaging; cancer therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mutein; human neutrophil gelatinase-associated lipocalin; hNGAL; rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin; 24p3; mutagenesis; fusion protein; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified hNGAL related fusion protein SEQ ID NO:20
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                                                                                                              27-SEP-2001; 2001WO-EP011213
16-APR-2002; 2002WO-EP004223
                                                                                                                                                                                                    18-SEP-2002; 2002WO-EP010490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                       (PIER-) PIERIS PROTEOLAB AG
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Schlehuber S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22. .400
/note= "modified hNGAL, Strep-tag II and phage coat
rrotein pIII fragment fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein pIII fragment 22. .199
                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amber stop codon"
211. 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "Strep-tag II affinity tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note= "mature hNGAL"
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                                                                                                                                                                                                                                                                                                                                                                               "coat protein pIII fragment 217-406"
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Pred. No. 0.098;
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CC given target, comprising subjecting the protein to mutagenesis at constituents 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in cc muteins of the protein. Also described: (1) a mutein of hNGAL, A2m or CC 2493 having detectable binding affinity to a given target, obtained by the method described above; (2) a fusion protein comprising the mutein of hNGAL, A2m or 2493, where an enzyme, a protein or a protein domain, a cc peptide, a signal sequence and/or an affinity tag is operably fused to the amino or carboxy terminus of the mutein of hNGAL, A2m or 2493 or the cc comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the fusion protein described above, and a carrier. The muteins have cytostatic activity, and can be used in c gene therapy. The method is useful in generating or producing a mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or the fusion protein is useful in generating or producing a mutein of hNGAL, A2m or 2493 or the fusion protein is useful in detecting a given target by contacting the mutein between the mutein and the given carget, and determining the complexed mutein by a suitable signal. The conditions that allow complex domain, a peptide, a nucleic acid molecule, an organic molecule or a metal complex and the detection is carried out for validation of the protein as a pharmacological drug target. The mutein may also be used in medicine, e.g. for tumour imaging cor directly for cancer therapy. The present sequence represents a modified hNGAL, Strep-tag II and phage coat protein pIII fragment fusion protein given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or m 24p3/uterocalin, comprises subjecting the protein to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocalin (hNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse 24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
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N-PSDB; ADA00706.
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                                Matches
                                       Query Match
Best Local (
 202
                               16;
               1 WSHPQFEK--GGGSGGS 16
                                        Similarity
WSHPQFEKQAGGGSGGGS
                                Conservative
                                        57.5%;
219
                              0
                                        Score 84; DB 6;
Pred. No. 0.098;
                                Mismatches
                                0
                                              Length 400
                                Indels
                               2;
                              Gaps
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Sequence

400 AA;

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RESULT 9
ADA00701
mutein; human neutrophil gelatinase-associated lipocalin; hNGAL; rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin; 24p3; mutagenesis; fusion protein; cytostatic; gene therapy;
                                                                 Homo
                                                                          Synthetic
                                                                                               tumour imaging; cancer therapy.
                                                                                                                                                     Modified hNGAL related fusion protein
                                                                                                                                                                           06-NOV-2003 (first entry)
                                                                                                                                                                                                  ADA00701;
                                                                                                                                                                                                                      ADA00701 standard;
                              Peptide
                                                              sapiens.
            1. .21
/label= signal
                                         Location/Qualifiers
                                                                                                                                                                                                                       protein; 400 AA
                                                                                                                                                      SEQ ID NO:14.
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Protein

22. .400
/note= "modified hNGAL, Strep-tag II and phage coat

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CC protein selected from a human neutrophil gelatinase-associated lipocalin CC (hNGAL), rat alpha2-microglobulin-related protein (Azm) and a mouse CC (24p3) therocalin (24p3), where the mutein has a detectable affinity to a CC given target, comprising subjecting the protein to mutagenesis at CC given target, comprising subjecting the protein to mutagenesis at CC gositions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in CC positions of the protein. Also described: (1) a mutein of hNGAL, AZm or CC the method described above; (2) a fusion protein comprising the mutein of the protein and row repair the mutein of the mutein of cc peptide, a signal sequence and/or an affinity to a given target, obtained by CC peptide, a signal sequence and/or an affinity tag is operably fused to CC peptide, a sequence encoding the mutein of hNGAL, AZm or 24p3 or the comprising a sequence encoding the mutein of hNGAL, AZm or 24p3 or the comprising a sequence of (2); and (4) a pharmaceutical composition comprising CC and a carrier. The muteins have cycostatic activity, and can be used in CC and a carrier. The muteins have cycostatic activity, and can be used in CC gene therapy. The method is useful in generating or producing a mutein of hNGAL, AZm or 24p3 or a fusion protein. The mutein given target under the fusion protein is useful in detecting a given target by contacting cor the fusion protein is useful in detecting a given target by contacting cor the fusion protein of containing the complex domain, a peptide, a nucleic acid conditions that allow complex formation between the mutein and the given target, and determining the complexed mutein by a suitable signal. The conditions that allow complex formation between the mutein and the given carried out for validation of the protein domain, a peptide, a nucleic acid conditions and conditions and the detection is modified hNGAL, Strep-tag II and phage coat protein invention.
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                                                                   Query Match
Best Local S
Matches 16
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16-APR-2002; 2002WO-EP004223
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associated lipocalin, rat alpha2-microglobulin-related protein or m
24p3/uterocalin, comprises subjecting the protein to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Skerra A, · Schlehuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 96-98; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PIER-)
                                                                                                                                              Sequence 400
202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIERIS PROTECLAB AG
                                                                                           Similarity
                                   WSHPQFEK--GGGSGGGS
                                                                         Conservative
                                                                                                                                                  ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Strep-tag II affinity tag"
210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein pIII fragment fusion protein"
22. .199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "mature hNGAL"
200. .209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211. .400
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                                                                                             57.5%;
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                                                                                             Score 84; DB 6;
Pred. No. 0.098;
                                                                               Mismatches
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metalloprotease;

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ADS20249
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB46427 standard; protein; 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel polypeptides (I) that are muteins of bilin-binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, have an arrival at the substitution at at least one of the positions 28, 13, 34-37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125 or 127, (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, separate Dig or the conjugates with proteins, nucleic acids, separates, other biological or synthetic macromolecules or low carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being used as a label. Compared with Dig-specific antibodies, (I) have a simpler structure and are easier to prepare. They have very high specificity for Dig, relative to other storoids, and fusion partners may be attached to either end without compromising their ability to bind light.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bilin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-JUN-2000; 2000WO-DE001873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200075308-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-071071/08.
N-PSDB; AAF25712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 72-74; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SKER/) SKERRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 659 AA;
                                                                                       Furin-processed human aggrecanase ADAMTS4 truncated protein w Strep tag
ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; reprolysin; zinc
                                                                                                                                                        18-NOV-2004
                                                                                                                                                                                                                                                                                ADS20249 standard; protein;
                                                                                                                                                                                                                         NDS20249;
                                                                                                                                                                                                                                                                                                                                                                                                                                 198 WSHPQFEKGGGGG 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WSHPQFEKGGGSG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlehuber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DE-01026068
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.4%;
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Pred. No. 1.8;
0; Mismatches
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RESULT 12
ADS20227
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Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity fo treating aggrecanase-associated conditions, including osteoarthritis.
              ADS20227 standard;
                                                                                                                                                                                             Sequence 485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-JUL-2002; 2002US-0398721P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JUL-2003; 2003WO-US023484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-FEB-2004
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Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aggrecanase; osteopathic; antiinflammatory; antiarthritic; antirheumatic; cytostatic; osteoarthritis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Croh's disease; human; chromosome 1q21-q23; enzyme; truncation; mature; furin cleavage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corcoran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004011637-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AMHP)
(CORC/)
(FLAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RACI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZENG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-143860/14.
                                                                                  456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) RACTE L A.
) MCDONAGH T.
) FREEMAN B A.
) GEORGIADIS K I
LAVALLIE E R.
                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORCORAN C
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ğ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZENG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HIBYW
                                                                                                            SHPQFEK-----GGGSGGGSWSHPQFEK 24
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 47;
                                                                                  SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK
                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flannery CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georgiadis
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/note= "Re
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             protein; 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            æ 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Residues corresponding to positions 687-837
wild-type replaced by Strep tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ы
                                                                                                                                                   49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  117pp;
                                                                                                                                   Score 71.5; DI
Pred. No. 3.3;
3; Mismatches
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Lavallie ER;
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                                                                                  485
                                                                                                                                                                  DB
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                                                                                                                                                                  Length 485;
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SHPQFEK---

----GGGSGGGSWSHPQFEK 24

Best Loc Matches Query Match

Local Similarity

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Conservative

Mismatches

Indels

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Gape

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668 SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK

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The invention relates to a novel isolated, modified ADAMTS4 (a disintegrin-like and metallogrotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAWTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAWTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The protein of the invention demonstrate osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of the human aggrecanase ADAWTS4 truncated protein with Strep tag of the invention.
                                                                                                                                                                                                                                                                                                                           New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity for treating aggrecanase-associated conditions, including osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aggrecanase; osteopathic; antiinflammatory; antiarthritic; antirheuma cytostatic; osteoarthritis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAMTS4; a disintegrin-like and metalloprotease;
thrombospondin type 1 motif 4; reprolysin; zinc metalloprotease;
                                         Sequence 697
                                                                                                                                                                                                                                                                                               Claim 9; SEQ ID NO 24; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                      Corcoran CJ, Freeman BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZENG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
Misc-difference 687. .697
/note= "Wild-type residues 687-837 replaced by Strep tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human aggrecanase ADAMTS4 truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADS20227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMHP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-2002; 2002US-0398721P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LAVA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FLAN/)
                                                                                                                                                                                                                                                                                                                                                                                        2004-143860/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCDONAGH T.
FREEMAN B A.
GEORGIADIS K 1
LAVALLIE E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORCORAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WYETH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZENG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RACIE L A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Georgiadis
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                                                                                                                                                                                                                                                                                                                                                                                                                      Flannery CR,
eorgiadis KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome 1q21-q23; truncation; Strep tag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M
49.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Zeng W, R
Lavallie
Score 71.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein with
                                                                                                                                                                                                                                                                                                                                                                                                                      Racie LA,
e ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Mcdonagh T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strep tag
            Length
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disintegrin-like and metallogrotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAMTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAMTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc metallogroteases and include aggrecanases amongst their members. The protein of the invention demonstrates osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of the human aggrecanase ADAMTS4 mutant E362Q protein with
                                                                                                                                                                                                                                                                               New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity for treating aggrecanase-associated conditions, including osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-143860/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Wild-type Glu substituted by Gln"
Misc-difference 520. .527
/note= "^"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers Misc-difference 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombospondin type 1 motif 4; reprolysin; zinc metalloprotease; aggrecanase; osteopathic; antiinflammatory; antiarthritic; antirheuma cytostatic; osteopathicis; glloma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADS20243 standard;
                                                                                                                                                                                                                   The invention relates to a novel isolated, modified ADAMTS4 (a
                                                                                                                                                                                                                                                    Claim 9; SEQ ID NO 40; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                               Freeman BA,
                                                                                                                                                                                                                                                                                                                                                                                              Corcoran CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2003; 2003WO-US023484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004011637-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human aggrecanase ADAMTS4 mutant E362Q protein with inserted Strep tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADS20243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JUL-2002; 2002US-0398721P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; enzyme; chromosome 1q21-q23; Strep tag; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; reprolysin; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLAN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                            MCDONAGH T.
FREEMAN B A.
GEORGIADIS K E
LAVALLIE E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORCORAN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RACIE L A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZENG W.
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Jeorgiadis KE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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Lavallie ER;
                                                                                                                                                                                                                                                                                                                                                                                              Mcdonagh T;
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                                                                                                        The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microtritre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor: (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                                                                                                                                                                                                                                                                                                                                         New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding modules.
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptavidin; protein chip; microtitre plate; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptavidin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                               Disclosure; Page 4; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-031166/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001DE-01013776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-OCT-2002.
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                              l Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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    WSHPQFEKGGGSGGGS-----WSHPQFEK
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                              47.3%;
nilarity 46.9%;
Conservative
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                          Score 69; us of Pred. No. 0.33 0; Mismatches
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Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID
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WSHPQFE-----KXXXXXXXXXXXHPQFEK

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                                                                                                                                                                                                     The invention relates to a method for producing a protein array made by CC transcription and translation of DNA, or by translation of mRNA, by a CC cell free system in vitro to produce individual proteins, domains or CC cell free system in vitro to produce individual proteins, domains or CC peptides distributed in a gridded format. The peptides of the invention CC contain amino acid sequences enabling covalent/non-covalent attachment to contain amino acid sequences enabling covalent/non-covalent attachment to contain amino acid sequences enabling covalent/non-covalent attachment to complete the grid format covalent interaction of the grid format covalent interaction of the grid format covalent for interactions of the covalent system is useful for identifying interactions of the covalent of the groteins or domains, peptides, small ligands, cell extracts and nucleic covalents. The protein array is also useful for identifying interactions of covalent protein array is arrayed protein with other molecules displayed in a library such as a covalent for studying cellular protein expression profiles and post-covalent in a protein array is considered to the covalent covalents a protein of a double hexahistidine with a flexible covalence of the covalence of the covalence and post-covalence covalence and post-covalence of the covalence of 
                                                                                                 Query Match
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Matches 13
                                                                                                                                                                                                     Sequence 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3B; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein arrays useful for identifying interactions of arrayed proteins with other molecules, in which proteins are produced by in vitro synthesis using cell-free transcription and translation systems.
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N-PSDB; AAK98912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He M,
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01-DEC-2000; 2000GB-00029309.
16-MAR-2001; 2001GB-0006610.
07-JUN-2001; 2001GB-00013883.
14-JUL-2001; 2001GB-00017232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein array; cell free system; gridded format; covalent; non-covalent; ligand, phage display library; cellular protein expression profile; ribosome display library; post-translational modification; hexahistidine; flexible linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAO19986 standard; protein; 42 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-AUG-2001; 2001WO-GB003657.
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                                                                                                                                                                                                                                                  linker sequence upstream
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                                                                                                                            Similarity
WRHPQFGGHHHHHHGGGSGGGS 31
                                               WSHPQF-----EKGGGSGGS 16
                                                                                                                                                                                                     $
                                                                                                    Conservative
                                                                                                 45.2%; Score 66; DB
59.1%; Pred. No. 1.3
:ive 0; Mismatches
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Search completed: March 2, 2005, 13:02:48 Job time : 109.098 secs

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Result
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Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpaa/US07_2: /cgn2_6/ptodata/2/pubpaa/PCT_N

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m2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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gn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
gn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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US-10-628-432-47
US-10-628-432-40
US-10-628-432-40
US-10-026-578B-3
US-10-034-607-16
US-10-036-578B-10
US-10-344-607-20
US-10-344-607-20
US-10-628-432-49
US-10-628-432-49
US-10-628-432-7
US-10-437-963-167129
US-09-977-137A-4
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                                                                                                                                                                                                                                                                  Description
                              Sequence 11, Appl
Sequence 47, Appl
Sequence 24, Appl
Sequence 30, Appl
Sequence 16, Appl
Sequence 10, Appl
Sequence 20, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
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RESULT 1

US-10-026-578B-11

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-10-437-963-18163	-437-963-15162	-10-437-96	-10-437-963-16111	-10-322-281-55	37-963-	-10-437-963-10841	-10-437-963-19305	-10-304-630-3	-10 - 8	887-228A-	-10-887-228A-	-10-437-	09-809-517A	09-809-5	-09-809-517A-3	09-809-517A-3	-10-728-246	-10-1	10-628-43	-10-358-283-1	-10-354-983-	-10-302-100B-	28-432-	-10-354-983-29	-10-437-963-	US-09-977-137A-6	-09-977-137A-1	-09-977-137F	•	US-09-977-137A-8	US-09-977-137A-7
Sequence 181639,	1516	Sequence 148362,	1611	"	.,	e 108	e 193	e 33,	Sequence 5, Appli	e 9,	equence 1,	161	Ę	Sequence 31, Appl	ω	30,	3 13,	•	Sequence 53, Appl	equence 15,	e 8, Appl	equence 41,	e 25, App	e 29, App	e 19	e 6, Appl	e 12	e 10, App	e 9, Appl	Sequence 8, Appli	e 7, Appl

# ALIGNMENTS

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CURRENT APPLICATION NUMBER: US/10/026,578B; CURRENT FILING DATE: 2002-11-11; PRIOR APPLICATION NUMBER: DE 101 13 776.1 PRIOR FILING DATE: 2001-03-21; PRIOR APPLICATION NUMBER: PCT/EP01/11846; PRIOR FILING DATE: 2001-10-12; NUMBER OF SEQ ID NOS: 14; SOFTWARE: Patentin version 3.1; SEQ ID NO 11
                                                                                 ; NAME/KEY: misc feature ; OTHER INFORMATION: Artificial Sequence represents peptide binding module US-10-026-578B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10026578B
Publication No. US20030083474A1
GENERAL INFORMATION:
APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILS REFERENCE: 100810.01US1
                                                                                                                                                                                FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (9)...(28)

OTHER INFORMATION: of the five (COTHER INFORMATION: repeats may be OTHER INFORMATION: be present
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
  80.1%;
  Score 117; DB 14; Pred. No. 1.5e-06;
                                                                                                                                                                                                               (GGGS) repeats between position 9 and 28, one or more be missing. However, at least one (GGGS) repeat will
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US-10-628-432-40
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US-10-628-432-24
                                                                                                         RESULT 4
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                                            Sequence 40, Application US/10628432 Publication No. US20040142863A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH. 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 24, Applicat Publication No. US200 GENERAL INFORMATION:
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Best Local Similarity
Matches 14; Conserv
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Best Local
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
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APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                              LENGTH: 697
TYPE: PRT
                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Truncated ADAMTS4 molecule
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No. US20040142863A1
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Pred. No. 3.
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Pred. No. 2.
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Sequence 3, Application US/10026578B

| Publication No. US20030083474A1 |
| GENERAL INFORMATION: |
| APPLICANT: IBA (GmbH) |
| APPLICANT: IBA (GmbH) |
| APPLICANT: Schmidt, Thomas |
| TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta |
| FILE REFERENCE: 100810.01US1 |
| CURRENT APPLICATION NUMBER: US/10/026,578B |
| CURRENT FILING DATE: 2002-11-11 |
| PRIOR APPLICATION NUMBER: DE 101 13 776.1 |
| PRIOR APPLICATION NUMBER: DE 101 13 776.1 |
| PRIOR APPLICATION NUMBER: DE 101 13 776.1 |
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CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 13; Conserv
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NAME/KEY: MISC FEATURE
TOCATION: (12)...(12)
TOWN: X F
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NAME/KEY: MISC FEATURE
TOTATION: (11)...(11)
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TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: X represents a single amino acid at the position indicated
                               NAME/KBY: MISC_FEATURE LOCATION: (15)..(15)
                                                                                                  LOCATION: (14)..(14)
OTHER INFORMATION: X represents
                                                                                                                                                                                                                     LOCATION: (13). (13)
OTHER INFORMATION: X represents
                                                                                                                                                                                                                                                                                                                     LOCATION: (12). (12)
OTHER INFORMATION: X represents a single amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MISC_FEATURE LOCATION: (10)..(10)
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OTHER INFORMATION: Synthetic Peptide
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ORGANISM: Artificial
                                                                                                                                             NAME/KEY: MISC FEATURE LOCATION: (14)...(14)
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OTHER INFORMATION: X represents
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LOCATION: (13)..(13)
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72.2%;
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Sequence 16, Application US/10344607
Publication No. US20040161748A1
GENERAL INFORMATION:
APPLICANT: HE, MINGYUE
APPLICANT: TAUSSIG, MICHAEL JOHN
ITITLE OF INVENTION: FUNCTIONAL PROTEIN ARRAYS
FILE REFERENCE: 37945-0049
CURRENT APPLICATION NUMBER: US/10/344,607
CURRENT FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US/10/3657
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 20
SOPPMAND: DATE: 201-08-15
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US-10-026-578B-10
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                                                                               APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
APPLICANT: Schmidt, Thomas
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity '
FILE REFERENCE: 100810.01US1
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
SUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 36
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SEQ ID NO 16
LENGTH: 42
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Best Local Similarity 46.9
Matches 15; Conservative
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Best Local
    FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: oligopeptide
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OTHER INFORMATION: Artificial Sequence represents
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                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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INFORMATION: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Pred. No.
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CURRENT APPLICATION NUMBER: US/10/344,607
CURRENT FILING DATE: 2003-02-13
PRIOR PRICHATION NUMBER: PCT/GB01/03657
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER NUMBER: POSSIBLE OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICIAL PROCESSION OF ARTIFICATION OF ARTIFICIAL PROCESSION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTIFICATION OF ARTI
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                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 49
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/10344607 Publication No. US20040161748A1 GENERAL INFORMATION:
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
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TITLE OF INVENTION: FUNCTIONAL PROTEIN ARRAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 37945-0049
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OTHER INFORMATION: ed; some of the amino acids may be missing. Where amino acids
OTHER INFORMATION: missing, the total numbers of x will be no less than 5
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NAME/KEY: MISC_FEATURE
LOCATION: (9)..(28)
OTHER INFORMATION: X re
OTHER INFORMATION: furin-processed construct
                                                                                                       LENGTH: 646
TYPE: PRT
                                        ORGANISM: Artificial FEATURE:
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OTHER INFORMATION: Artificial Sequence represents peptide binding module
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Pred. No. 2.
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RESULT 10
US-10-628-432-27
Sequence 27, Application US/10628432
Publication No. US20040142863A1
Publication No. US20040142863A1
GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AMI01378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTMARE: PatentIn version 3.1
SEQ ID NO 27
SEQ ID NO 27
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                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_65770C.1.pep
US-10-437-963-167129
                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 167129
LENGTH: 929
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Best Local :
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Best Local Similarity
                                                              Matches
                                                                                            Query Match
                                                                                                                                                                                                                                                       APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-2118

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14
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ORGANISM: Artificial
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                                                                                                                                                                          ORGANISM: Oryza sativa
                                                                                                                                                           FEATURE:
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                                                                           Local Similarity
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                            WSHPQFEKGGGSGGGSW 17
WRSPAMDHGGGGGGGVW 553
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Pred. No.
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Pred. No.
                                                                           Score 61; DB 16; Length 929; Pred. No. 67;
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RESULT 14 US-09-977-137A-7

Sequence 7, Application US/09977137A publication No. US20030104524A1 GENERAL INFORMATION:

APPLICANT: Summers,

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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-977-137A-4
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US-09-977-137A-4
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO.4
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                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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Best Local Similarity
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 79-00
                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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es 11; Conservation
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KGNVSCPSAWSHPQFEK 117
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APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Methods
FILE REFERENCH: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGOTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: chelon
US-09-977-137A-8
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CURRENT APPLICATION NUMBER: US/09/977,137A

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/240,465

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 7

SEQ ID NO 7

TYPE: PRT

ORGANISM: Artificial Sequence
PEATURE:
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: chelon
US-09-977-137A-7
Search completed: March 2, 2005, 14:18:52 Job time: 74.6341 secs
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US-09-977-137A-8
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Best Local Similarity 64.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cáguiat, Jonathan TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION: Methods
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

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Sequence 4, Application US/09977137A

Patent NO. 6750042

GENERAL INFORMATION:

APPLICANT: Summers, Anne O.

APPLICANT: Caguiat, Jonathan

ITILE OF INVENTION: Metal Binding Proteins, R.

ITILE OF INVENTION: Methods

FILE REFERENCE: 79-00

CURRENT APPLICATION NUMBER: US/09/977,137A

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/240,465

PRIOR APPLICATION NUMBER: US 60/240,465

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 4

LENGTH: 117

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

CRUET INFORMATION: Description of Artificial
                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: chelon US-09-977-137A-4
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US-09-977-137A-5
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Best Local Similarity
Matches 11; Conserv
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION INMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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PCT-US95-09816A-97
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US-09-270-767-3351
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US-09-809-517A-27
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Query Match

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Title:

SEQ11 146

Scoring table:

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24, Appl 27, Appl 17127, A 42, Appl 60227, A 26, Appl 44768, A 17780, A

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                                                                                        SEQ ID NO 8
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Patent No. 6750042
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Best Local
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
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                                                                                                                       PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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Best Local Similarity
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                       APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                          APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
                                                                                                        SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                          FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
     OTHER INFORMATION:
                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                        FEATURE:
                                                          TYPE: PRT
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ORGANISM: Artificial Sequence
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                                                                        ENGTH: 117
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Description of Artificial Sequence:
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Pred. No. 3.2;
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US-09-977-137A-9
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEO ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 10
                                                           Matches
                                                                         Query Match
Best Local :
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APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonath
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APPLICANT: Summers,
APPLICANT: Caguiat
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Best Local Similarity
Matches 11; Conserv
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Patent No. 675004
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                            LENGTH: 11
TYPE: PRT
                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                          FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: chelon
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KGNVSCPSAWSHPQFEK 117
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                                                          Conservative
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Pred. No.
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US-09-407-687-41
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Sequence 41, Application US/09407687 Patent No. 6548634 GENERAL INFORMATION:
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SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
LENGTH: 118
TYPE: PRT
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Best Local Similarity
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
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                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: chelon
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TYPE: PRT
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Pred. No.
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Pred. No. 3.2;
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US-09-809-517A-30
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SEQ ID NO 30
LENGTH: 21
                                                     Sequence 33, Application US/09809517A
Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly) peptides/proteins
TITLE OF INVENTION: particles via disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 39.7
Best Local Similarity 68.8
Matches 11; Conservative
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/407,687
CURRENT FILING DATE: 1999-09-28
EARLIER APPLICATION NUMBER: 60/102,667
EARLIER FILING DATE: 1998-09-30
NUMBER OF SEQ ID NOS: 43
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APPLICANT: Kavanaugh, Michael
TITLE OF INVENTION: Synthetic Peptides Having FGF Receptor
TITLE OF INVENTION: Affinity
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CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
                                      FILE REFERENCE: MORPHO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE: OTHER INFORMATION: synthetic peptide
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ORGANISM: Syartificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: synthetic module
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Pred. No.
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Pred. No. 1
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US-09-809-517A-34
; Sequence 34, Application US/09809517A
; Patent No. 6753136
; Patent No. 6753136
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Best Local Similarity
Watches 9; Conserve
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US-09-809-517A-33
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conser
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly) peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                GENERAL INFORMATION:
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Patent No. 6753136

GENERAL INFORMATION:

APPLICANT: Lohning, Corinna

TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on TITLE OF INVENTION: particles via disulfide bonds

PILE REFERENCE: MORPHO//1
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CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR FILING DATE: 2000-02-18 NUMBER OF SEQ ID NOS: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic module
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TYPE: PRT
ORGANISM: artificial sequence
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81.8%; Pred. No.
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RESULT 15
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Best Local Similarity
Watches 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-34
                                                                                                                                                                                                                                                                                                                                      Sequence 2, Apra-
Sequence 2, Apra-
No. 5814503
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SEQ ID NO 33
LENGTH: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6534036
GENERAL INFORMATION:
APPLICANT: D-Gen Limited
TITLE OF INVENTION: BIOLOGICAL MATERIALS AND METHODS USEFUL
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF PRION DISEAS
FILE REFERENCE: ICOT/P21952
CURRENT APPLICATION NUMBER: US/09/431,887
CURRENT FILING DATE: 1999-11-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Kovacevic, Steven
APPLICANT: Otto, Keith A.
APPLICANT: Rao, Ramachandra N.
TITLE OF INVENTION: FUSION PROTEINS COMPRISING CELL CYCLE
TITLE OF INVENTION: REGULATORY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: GB 9824091.4 PRIOR FILING DATE: 1999-11-04 NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                           ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                   COUNTRY:
APPLICATION NUMBER:
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653405
WAT
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                                                                                                                                 USA
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US/08/770,761A
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Pred. No. 1.5;
0; Mismatches
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Pred. No. 17;
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FILING DATE: 19-DEC-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10136
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-376-0756
TELEPHONE: 317-277-1917
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 amino acids
TYPE: maino acids
TYPE: maino acids
TYPE: maino acids
TYPE: molinear
MOLECULE TYPE: peptide
US-08-770-761A-2
                                                                                               밁
Search completed: March 2, 2005, 12:25:36 Job time: 27.3171 secs
                                                                                                                                                                                    Query Match 38.4%; Score 56; DB 2; Length 660; Best Local Similarity 50.0%; Pred. No. 44; Matches 8; Conservative 3; Mismatches 5; Indels
                                                                                       7 EKGGGSGGSWSHPQF 22
::| || :| || || 643 DEGNPEGGSAWRHPQF 658
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Page 5

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Copyright

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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OM protein - protein search, using sw model
                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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PIR_79:*
1: pir1:*
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                                                                                                                                                                                                                                                   96216763 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIE

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597 :	597							430 :																		629 2			Length DB
2 AE0721			1 YRMSB6	YRHUB	2 T32991	2 AH1126		2 AH3420			2 C86570			2 JQ1021			2 AH1117		G81								2 T23175		a Ib
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oligo-1,6-glucosi	2 T30268	34 :	U	45.5	50	45
	2 C87349	467 :	4	45.5	50	44
	2 A39172	34 :	ω	45.5	50	43
	2 C84701	10 ::	ω	45.5	50	42
	2 AH3479	84 :	N	45.5	50	41
	2 AD2758	77 ;	N	45.5	50	40
	2 A97539	77 ;	N	45.5	50	39
	T08785	43	ผ	45.5	50	38
	2 A90904	8	<b></b>	45.5	50	37
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	P T15232	18	14	46.4	51	32
	2 A90770	97 ;	597	46.4	51	31
	E85632	97	ú	46.4	5	30

# ALIGNMENTS

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R;Sims, M.

RySims, M.

Bubmitted to the EMBL Data Library, April 1995
A;Reference number: Z19702
A;Accession: T23175
A;Status: translated from GB/EMBL/DDBJ
A;Residues: Lype: DNA
A;Residues: 1-650 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein K01C8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23175
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T23175
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A;Molecule type: DNA
A;Residues: 1-298 -KUR>
A;Cross-references: UNIPROT:Q99SV5; GB:BA000018; PID:g13701726; PIDN:BAB43019.1; GSPDB:G
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: D89982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SA1747 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: D89982
                                        A;Map position: 2
A;Introns: 31/1; 74/1; 181/3; 392/2; 416/1; 489/3; 551/1
F;78-546/Domain: animal histidine decarboxylase homology <HDC>
                                                                                                                                           A;Cross-references: UNIPROT:Q21087; EMBL:Z49068; PIDN:CAA88862.1; A;Experimental source: clone K01C8 C;Genetics:
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                                                                                                                    A; Gene: CESP: K01C8.3
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WITKQLEKMIAPFYRKWDHQVFE 112
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     51.8%; Score 57;
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Pred. No.
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A54660
histidine rich c
C;Species: Homo
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Nature 399, 323-329, 1999

A;Title: Evidence; for lateral gene transfer between Archaea and reafarence number: A72200; MUID:99287316; PMID:10360571
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A;Residues: 1-385 <ARN>
A;Cross-references: UNIPROT:09X2A5; GB:AE001816; GB:AE000512; NID:g4982359; PIDN:AAD3684
A;Experimental source: strain MSB8
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                                                             RESULT
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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, N.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre
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Matches
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9; Mismatches
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ribosomal protein S17 TC0806 [imported] - Chlamydia muridarum (£ C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Jate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change C;Accession: F81664 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J, C.; Dodson, R.; Gwinn, M.; Naler, "
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C; Superfamily: Escherichia co... C; Keywords: protein biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Cloning and sequence analysis of the Chlamydia A;Reference number: A42645; MUID:92138612; PMID:1735714 A;Accession: C42645
                                                                                                                                                                                               A;Gene: rs17
                                                                                                                                                                                                                                  A;Cross-references: GB:AE001323; GB:AE001273; NID:g3328931; A;Experimental source: serotype D, strain UW-3/Cx
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A; Residues: 1-83 < ARN>
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A;Accession: E71506
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A; Residues: 1-83 < KAU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ribosomal protein S17 - Chlamydia trachomatis
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A;Map position: 19q13.3-19q13.3
C;Keywords: calcium binding
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A; Residues: 1-699 < HOF >
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                                                                                                                                                        Superfamily: Escherichia coli ribosomal protein; Keywords: protein biosynthesis; ribosome
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7; Conserv
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                                     WSHPOFEKXXXXXXXXXXXSHPOFE 23
YSHPQYAKVVRDSSKYYAHNELD 55
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Heidelberg, J.F.; White, O.
; Kolonay, J.; McClarty, G.;

o ::

; Hickey, Salzberg,

(strain Nigg)

09-Jul-2004

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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-147 <KUR>
A;Cross-references: UNIPROT:Q99VU5; GB:BA000018; PID:g13700567; PIDN:BAB41864.1; GSPDB:
                                                                                                                                                                                                                                                    C;Accession: E89838

R;Kuroda, M.; Ohte, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: E89838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Schmutzler, C.; Darmer, D.; Diekhoff, D.; Grimmelikhuijzen, C.J. J. Biol. Chem. 267, 22534-22541, 1992
A;Title: Identification of a novel type of processing sites in the A;Reference number: A44308; MUID:93054550; PMID:1429603
A;Accession: A44308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antho-RFamide precursor - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44308
                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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C; Superfamily:
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A;Experimental source: strain Nigg (MoPn)
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A; Residues: 1-83 < TET>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA; protein A; Residues: 1-435 <SCH>
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  Query Match
Best Local S
Matches 8
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Best Local Similarity
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h 48.2%;
Similarity 33.3%;
8; Conservative
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Score 53; DB
Pred. No. 13;
9; Mismatches
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Pred. No.
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                                              Length 147;
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                     RESULT 12
AH1117
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C;Accession: H96765
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; annen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000
R;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

R;A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Recession: H96765
R,Sternen: H96765
R,Sternen: H96765
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G81305
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                                                                            Query Match
Best Local Similarity
""" hes 8; Conserv
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A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-268 < PAR>
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A;Accession: G81305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: G81305
R;Parkhill, J.; Mren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable dnaJ-like protein Cj1034c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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A; Map position: 1
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A; Residues: 1-338 < STO>
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                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q9C9S8; GB:AE005173; NID:g6692747; PIDN:AAF24853.1; GSPDB:GN
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Best Local S
Matches 7
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101
FSHPQRQGHLNPAVTSMSHPQ
                                                 WSHPQFEKXXXXXXXXXXXXXXXX 21
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31.8%; Pred. No.
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38.1%; Pred. No.
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transaldolase homolog lmo0343 [imported]

Listeria monocytogenes (strain EGD-e)

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C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH1117
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker pominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L. M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Matheristive genomics of Listeria species
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AH1117
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A;Residues: 1-218 <GLA>
A;Cross-references: UNIPROT:Q92EU7; GB:NC_003210;
A;Experimental source: strain EGD-e
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AB1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transaldolase homblog lin0361 [imported] - Listeria innocua (strain Clip11262) C;Species: Listeria innocua (c;Species: Listeria innocua (c;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004 C;Accession: AB1478
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                                                                                                RESULT 14
C084904
hypothetical protein At2g46550 [imported] - Arabidopsis thaliana
C;Secies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84904
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C; Superfamily:
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A;Residues: 1-218 <GLA>
A;Cross-references: UNIPROT:Q92EU7; GB:AL592022; PIDN:CAC95594.1;
A;Experimental source: strain Clip11262
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                   C;Accession: C94904

R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Ceuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Ceuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Ceuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C.
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Nature 402,
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Search completed: March Job time : 19.3415 secs

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2005, 12:28:58

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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: C84904 A;Atatus: preliminary A;Status: preliminary A;Molecule type: DNA A;Residus: 1-397 <STO> A;Residus: 1-397 <STO> A;Cross-references: UNIPROT:Q9ZPY4; GB:AE002093; NID:g4415936; PIDN:AAD20166.1; G
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C;Species: Saccharomyces cerevisiae
A;Variety: Saccharomyces carisbergensis NCYC396
C;Date: 17-Jul-192 #sequence_revision 17-Jul-19
C;Accession: JQ1021
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A;Gene: At2g4655
A;Map position:
                                                                                                                                                                                                                                                                                                      Gene 101, 97-104, 1991
A;Title: Cloning, sequence and chromosomal A;Reference number: JQ1021; MUID:91285441; A;Accession: JQ1021
A;Molecule type: DNA A;Residues: 1-471 < TUR>
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A;Note: the source is designated as Saccharomyces carlsbergensis
C;Comment: Yeast strains producing this enzyme are able to use melibiose as a
                                                                                                                                       A;Map position: 10
C;Superfamily: alpha-galactosidase
C;Keywords: glycosidase; hydrolase
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Copyright (c) 1993 - 2005 Compugen Ltd.
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ATP-binding; Complete proteome.
SPOITEMER 208 AB. 1.
-1-SIMILARITY: Belongs to the EMBL; APO03363; BABS0095.1; - BYR; D89982; D89982; D89982; G0; G0:0016020; C:membrane; I:G0; G0:00016524; F:ATP binding G0; G0:00042626; F:ATPseas activated of G0:00004626; F:mucleotide G0; G0:0006298; F:mucleotide G0; G0:0006298; F:mismatch rej G0; G0:0006810; P:transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99SV5 PRELIMINARY; PRT; 298 AA.
Q99SV5;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to ABC transporter (ATP-binding protein).
OrderedLocusNamesesANJU33;
OrderedLocusNamesesANJU33;
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

STRAIN-MALSO / ATCC 700699;

MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,

Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus (strain Mu50 / ATCC 700699). Bacteria; Firmicutes; Bacillales; Staphylococcus. NCBI_TaxID=158878;
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                                                                                                                                                                                                                                                                                Lancet 357:1225-1240(2001).
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EMBL; AP004828;
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GO:0016020; C:membrane; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0045264; F:ATPase activity, coupled
GO:0003684; F:damaged DNA binding; IEA.
GO:0000166; F:nucleotide binding; IEA.
GO:0006298; P:mismatch repair; IEA.
GO:0006810; P:transport; IEA.
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GO:0005524; F:ATP binding; IEA.
GO:0045264; F:ATPase activity, coupled
GO:0003684; F:damaged DNA binding; IEA.
GO:0000166; F:nucleotide binding; IEA.
GO:0006298; P:mismatch repair; IEA.
GO:0006810; P:transport; IEA.
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8; Conser
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F:ATP binding; IEA.
F:ATPase activity, coupled to transmen
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34532 MW;
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9; Mismatches
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Best Local S
Matches 8
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-[- SIMILARITY: Belongs to the ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC transporter fan ABC GO: GO:000628; F:ANTPASE ABC transporter fan ABC GO: GO:000628; F:ANTPASE ABC BO: GO:0006298; F:MICHOELEGE BO: GO:0006298; F:MICHOELEGE BO: GO:0006298; F:MICHOELEGE BO: GO:0006298; F:MICHOELEGE BO: GO:GO:0006810; F:TRANSPORTER FAN ATPASE.

InterPro: IPRO3593; AAA ATPASE.
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InterPro; IPR003439; ABC_transporter.
InterPro; IPR003439; Mut5 C.
Pfam; PF00005; ABC_tran; I.
ProDom; PD000006; ABC_tran; E.
ProDom; PD0010363; Mut5 C; 2.
SMART; SM00382; AAA; 1.
PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
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SEQUENCE FROM N.A.

MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2; Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M., Yamashita A., Oshima K., Furnya K., Yoshino C., Shiba T. Kanehisa M., Ogaaawara N., Hayashi H., Hiramatsu K., Hayashi H., Hiramatsu K.;

"Whole genome sequencing of meticillin-resistant Staphylococcus
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Q7A4N3;
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                                                               ProDom; PD000006; ABC transporter; 1. ProDom; PD001263; Mut5 C; 2. SMART; SM0382; AAA; 1.
                                                                                                                                                           PROSITE; PS50893; ABC_TRANSPORTER_2;
ATP-binding; Complete_proteome.
SEQUENCE 298 AA; 34439 MW; 6FAAE:
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                                                                                                                                                                                                                                                                                                                      Pfam; PF00005; ABC
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003439; ABC transporter.
InterPro; IPR000432; MutS C.
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SEQUENCE 298 AA; 34439 MW;
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WITKQLEKMIAPFYRKWDHQVFE 112

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RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Holden M.T.G., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Churcher C., Lark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Comond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RA Spratt B.G., Parkhill J.;
RT "Complete ginomes of two clinical Staphylococcus aureus strains:
RT "Complete ginomes of two clinical Staphylococcus aureus strains:
RT "Complete ginomes of two clinical Staphylococcus aureus strains:
RT "Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
C. -!- SIMILARITY: Belongs to the ABC transporter family.

EMBL; BX571857, CAG43662.1; --
DR GO; GO:0016420; C.membrane; IEA.
GO; GO:0016420; C.membrane; IEA.
GO; GO:0001652; F.ATP binding; IEA.
GO; GO:000166; F.inucleotide binding; IEA.
GO; GO:000166; F.inucleotide binding; IEA.
GO; GO:000691; p.transport; IEA.
GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000691; p.transport; IEA.

GO; GO:000692; AAC, TRANSPORTER_2; 1.

RMATT; SN00383; AAC_transporter; 1.

BOR ProDom; PD001263; MutS_C:
GO; GO:0006903; ABC_transporter; 1.

GO; GO:0006903; ABC_transporter; 1.

GO; GO:0006903; ABC_transporter; 1.

GO; GO:0006903; ABC_transporter; 1.

GO; GO:0006903; ABC_transporter; 1.

GO; GO:0006903; ABC_transporter; 1.

GO; GO:0006903; ABC_transporter; 1.

GO; GO:
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Best Local :
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Q6GFC4;
                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
putative ABC transporter ATP-binding protein.
OrderedLocusNames=SAR2025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative ABC transporter ATP-binding protein. OrderedLocueNames=SAS1857;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
SEQUENCE FROM N.A.
PubMed=15213324; DOI=10.1073/pnas.0402521101;
Holden M.T.G., Feil E.J., Lindsay J.A., Peaco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6G800;
                                                                                                                                                                 Staphylococcus aureus Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococque aureus (strain MSSA476).
Bacteria: Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6G800
                                                                                                                            NCBI_TaxID=282458;
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53.6%;
                                                                                                                                                                 (strain MRSA252).
Bacillales; Staphylococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB Pred. No. 24; 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
                                                                                                                                                                                                                                                                                                                                                                                                                              298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
      Peacock S.J.,
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      Day N.P.J.,
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Belongs to the ABC transporter fam
EMBL; BX571856; CAG41010.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0003684; F:ATPase activity, coupled to tran
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
GO; GO:0006298; P:mismatch repair; IEA.
GO; GO:0006298; P:mismatch repair; IEA.
GO; GO:0006310; P:transport; IEA.
InterPro; IPR003593; AABC transporter.
InterPro; IPR003439; ABC transporter.
InterPro; IPR000432; MutS_C:
PFODom; PD000005; ABC transporter; 1.
PFODom; PD001263; MutS_C: 2.
SWART; SM00382; AAA; 1.
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MATK_MARSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A., Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L., Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K., James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K., Ormond D., Quail M.A., Rabbinowitsch E., Rutherford K.M., Sanders M., Charles G., Gimmand M., Rabbinowitsch E., Rutherford K.M., Sanders M., Charles G., Gimmand M., Rabbinowitsch E., Rutherford K.M., Sanders M., Charles G., Gimmand M., Rabbinowitsch E., Rutherford K.M., Sanders M., Charles G., Gimmand M., Rabbinowitsch E., Rutherford K.M., Sanders M., Charles G., Gimmand M., Rabbinowitsch E., Rutherford K.M., Sanders M., Charles G., Gimmand M., Rabbinowitsch G., Barrell B.G.
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch)
                                                                            This SWISS-PROT entry is copyright. It is produced the between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no the European Bioinformatics Institute.
                                                                                                                                                                                                                                               "Phylogenetic relationships of the aquatic angiosperm family Podostemaceae inferred from matK sequence data."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Podostemaceae; Marathrum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8WKK9;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genomes of two clinical Staphylococcus aureus evidence for the rapid evolution of virulence and drug proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sharp S., Simmonds M., Stevens K., Whitehead S., Spratt B.G., Parkhill J.;

    -!- FUNCTION: Probably assists in splicing chloroplast group introns (By similarity).
    -!- SIMILARITY: Belongs to the intron maturase family 2. Matk

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=matK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maturase K (Intron maturase).
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Kita Y., Kato M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marathrum schiedeanum.
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                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=116737;
                                                                                                                                                                    subfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |: | ||:::::::| | || || WITKQLEKMIAPFYRKWDHQVFE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 44, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.6%; Score 59; DB 34.8%; Pred. No. 24; :ive 9; Mismatches
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                                                                                                       collaboration -
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ID Q9BB
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Best Local S
Matches 8
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                            "Infrafamilial Phylogeny of the Aquatic An Inferred from the Nucleotide Sequences of Plant Biol. 3:156-163 (2001).

EMBL, AB048378; BAB33398.1; -.

GO; GO:0009507; C:chloroplast; IEA.
GO; GO:0009508; P:RNA splicing; IEA.
InterPro; IPR00898; Agglutinin.
InterPro; IPR00842; Intron maturse2.
InterPro; IPR00846; MatK.N.
                                                                   O9BBG3;
Q9BBG3;
01-JUN-2001 (TremBLrel. 1
01-JUN-2001 (TremBLrel. 1
01-MAR-2004 (TremBLrel. 2
                                  Maturase K.
Name=matK;
Oserya coulteriana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BBG0;
01-JUN-2001
01-JUN-2001
01-MAR-2004
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
                          Chloroplast.
                                                                                                                                                                                                                                                                              Pfam; PF01348; Intron_maturas2; 1. Pfam; PF01824; MatK_N; 1. Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Podostemaceae; Vanroyenella.
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InterPro; IPR008998; Agglutinin.
InterPro; IPR000842; Intron maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maturase K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=51609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vanroyenella plumosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9BBG0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast; mRNA processing. SEQUENCE 508 AA; 61342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Kita Y., Kato M.;
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nilarity 42.1%;
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Kita Y., Kato M.;

"Infrafamilial Phylogeny of the Aquatic Inferred from the Nucleotide Sequences Plant Biol. 3:156-163(2001).

EMBL; AB048375; BAB33395.1; -...
GO; GO:0009507; C:chhoroplast; IEA. GO; GO:0008380; P:RNA splicing; IEA. InterPro; IPR008998; Agglutinin.

InterPro; IPR008966; MatK.N.

InterPro; IPR002866; MatK.N.
  01-MAR-2001
01-MAR-2001
01-OCT-2003
                                  Q9H7M8;
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Q8CJD2;
01-MAR-2003
01-MAR-2003
                                                                                                                                                                                       Lyase.
SEQUENCE
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Nakamura I., Suzuki N.;
Nakamura I. Suzuki N.;
Submitted (NOV-2002) to the
EMBL; AB096020; BAC24016.1;
HSSP; P30803; 1AZS.
                                                                                                                                                                                                                                 GO; GO:0004383; F:guanylate cyclase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0007242; F:ltracellular signaling cascade;
InterPro; IPR001054; G cyclase.
Pfam; PF00211; Guanylate cyc; 1.
SMART; SM00044; CYCc; 1.
                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                         PROSITE; PS00452; GUANYLATE_CYCLASES_1; PROSITE; PS50125; GUANYLATE_CYCLASES_2;
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01-MAR-2003 (TrEMBLrel. 25, Last
01-CCT-2003 (TrEMBLrel. 25, Last
Guanylyl cyclase alpha 1 subunit.
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SEQUENCE 508 AA;
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MCBI_TaxID=51602;
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nilarity 42.1%;
Conservative
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RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakami K., Yasuda T., Kuruya T., Kikkawa E., Omura Y.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Pujimori K.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momilyama H., Satoh N., Takami S., Terashima Y., Suuki O.,
RA Moriya S., Momilyama H., Satoh N., Takama S., Fukusa S.,
Pujimori Y., Yamada K., Fuji Y., Ozaki K., Hirao M., Ohmori Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fuji Y., Ozaki K., Hirao M., Ohmori Y.,
RA Misajama Y., Matuno T., Morinaga M., Sasaki M.,
RA Misushima S., Jasaki M., Matsuho T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Misushima S., Jasaki M., Matanabe T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Misushima S., Sadach T., Nakamaya M., Sasaki M.,
RA Misushima S., Sadach T., Nakama M., Sasaki M.,
RA Misushima S., Jasaki M., Matanaba M., Hata H., Watanabe M., Komatsu T.,
RA Misushima S., Jasaki M., Matanabita R., Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Nakagawa K.,
RA Misushima S., Jasaki M., Matanaba M., Sasaki M.,
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Q88PY3;
01-JUN-2003
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01-MAR-2004 (TrEMBLrel. 26, La
Outer membrane efflux protein.
OrderedLocusNames=PP0715;
                                                                      Pseudomonas putida (strain KT2440)
Bacteria; Proteobacteria; Gammapro
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Mammalia; Eutheria;
 SEQUENCE FROM N.A
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PRINTS; PR00449; RASTRNSFRMNG.
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                                                          Pseudomonadaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L; AK024450; BAB15740.1; -. GO:0005925; F:GTP binding; GO:0007264; P:small GTPase erPro; IBR001806; Ras_trnsfr
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                                                          Pseudomonas
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Primates;
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24, Last sequence update)
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                                                                        Gammaproteobacteria; Pseudomonadales;
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Pred. No.
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mediated
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Q21087;
Q1-NOV-1996
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01-JAN-1999 (TrEMBLrel. 09, Last sequence update
01-MAR-2004 (TrEMBLrel. 26, Last annotation upda
Hypothetical protein K01C8.3a.
Name=tdc-1; Synonyms=K01C8.3a; ORFNames=K01C8.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nelson K.B., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H., Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M., Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M., Hance I., Chris Lee P., Holtzapple B.K., Scanlan D., Tran K., Moazcez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S., Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                  GO; GO:0016831; F:carboxy-lyase activity; IEA.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0006520; P:amino acid metabolism; IEA.
InterPro; IPR010977; Aromatic dec.
InterPro; IPR002129; Pyridoxal dec.
Pfam; PF00282; Pyridoxal dec; 1.
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PIR; T23175; T23175.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                 WormBase; WBGene00006562; tdc-1.
WormPep; K01C8.3a; CE21011.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   investigating biology.";
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02321; OEP; 2
TIGRFAMs; TIGR01845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE016776; AAN66340.1; TIGR; PP0715; -.
                                                                                                                                                                                                                                                       HSSP; P80041; 1JS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22423060; PubMed=12534463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22
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Last annotation update)
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RESULT 15
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Hypothetical protein; Lyase; Pyridoxal phosphate.
SEQUENCE 650 AA; 73201 MW; 4830EECAFD14FAB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical conserved protein.
OrderedLocusNames=OB2578;
Oceanobacillus iheyensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22220767; PubMed=12235376; DOI=10.1093/nar/gkf526; Takami H., Takaki Y., Uchiyama I.; "Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme environments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QBENA9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95ZS2;
Q95ZS2;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
11-yoothetical protein K01C8.3b.
Name=tdc-1; Synonyms=K01C8.3b; ORFNames=K01C8.3;
Caenorhabditis elegans.
Cukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Eukaryota; Metazoa; Nematoda; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, AP004601, BAC145341; ...
InterPro; IPR004879; DUF255.
InterPro; IPR008928; Glyco_trans_6hp.
Pfam; PF03190; DUF255; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome; Hypothetical protein.
SEQUENCE 691 AA; 79588 MW; 11EP02E2445B06E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 30:3927-3935 (2002).
                                                "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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7; Conserv
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WSHPQFEKXXXXXXXXXXSHPQFEK 24
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Pred. No.
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Pred. No. 1.2e+0;
8; Mismatches
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Mismatches 1
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Matches 7
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WormBase; WBGene0006562; tdc-1.

WormBep; KO1C8.3b; CE28344.

GO; GO:0016831; F:carboxy-lyase activity; IEA.

GO; GO:0016829; F:lyase activity; IEA.

GO; GO:0006520; P:amino acid metabolism; IEA.

GO; GO:0006520; P:amino acid metabolism; IEA.

InterPro; IPR010977; Aromatic deC.

InterPro; IPR010977; Pyridoxal_deC.

pfam; PF00282; Pyridoxal_deC; 1.

pRINTS; PR00800; YHDCRBOXLASE.

PRINTS; PR00800; YHDCRBOXLASE.

PROSITE; PS00392; DDC GAD_HDC YDC; 1.

PROSITE; PS00392; DDC GAD_HDC YDC; 1.

PROSITE; PS00392; DDC GAD_HDC BBBDFD83582FEC6

SEQUENCE 705 AA; 79710 MW; B8BBDFD83582FEC6
                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
 136
                         6 FEKXXXXXXXXXXHPQF 22
                                              Similarity
7; Conserv
 FEKLIMPGITHWQHPRF 152
                                                  Conservative
                                                             51.8%;
                                                   9;
                                                               Score 57;
Pred. No.
                                                                                                   yridoxal phosphate.
B8BBDFD83582FEC6 CRC64;
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                                                                 DB 2; I
1.2e+02;
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Search completed: March 2, 2005, 12:44:26 Job time : 91.1707 secs

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Minimum DB
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Copyright (c) 1993 - 2005
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

659 4 AAB46426 Aab6 659 4 AAB46427 Aab6 199 7 ADB87309 Adbe 248 7 ADB87310 Adb6	63 57.3 659 4 AAB46426 63 57.3 659 4 AAB46427 62 56.4 199 7 ADB87309	63 57.3 659 4 AAB46426 AAb4663 57.3 659 4 AAB46427 Aab4	63 57.3 659 4 AAB46426 Aab4		63 57.3 448 4 AAB46425 Aab4	63 57.3 396 4 AAB46423	63 57.3 396 4 AAB46420	63 57.3 396 2 AAW93966	63 57.3 254 4 AAB46421	63 57.3 254 2 AAW93969	63 57.3 205 2 AAW93967	64 58.2 118 5 AAU97554	64 58.2 117 5 AAU97560	64 58.2 117 5 AAU97552 Aaus	64 58.2 117 5 AAU97556 Aaus	64 58.2 117 5 AAU97555 Aau9	64 .58.2 117 5 AAU97559 Aau9	58.2 117 5 AAU97557 Aau9	64 58.2 117 5 AAU97553 Aau9	58.2 117 5 AAU97558 Aau9	85.5 36 6 ABP60370 Abp603	.5 85.9 35 6 ABP60369 Abp603	6 ABP60362 Abp603	lt Query o. Score Match Length DB ID
	Apoli	905/	6427	6426 Bilin	5 Bilin	Bilin	0 Bilin	5 Plasmi	_	φ	7	4	Aau97560 Synthetic	7552 Synthet	7556	7555 Synthet	7559	7557	7553	7558 Sy	0370	0369 St	Abp60362 Streptav	scription

	AC ABP	RESULT 1 ABP60362 ID ABP6		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
28-MAR-2003	ABP60362;	0362		59	59	59	59	59	59.5	60	60	60	60	60	61	61	61	61	61	61	61	61	61.5
(first		standard; peptide;		53.6		53.6	•	•	•	54.5					•	•			•	•	•	٠	•
: entry)		peptid		19	19	19	19	19	633	858	772	763	199	646	467	400	400	400	400	400	183	183	697
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		24 AA.	ALIGNMENTS	ADI39155	ADI39157	ABG74880	ABG74882	ABG74881	ADS20255	ADS20230	ADP87577	ADB85492	AAE38369	ADS20251	ADP18461	ADA00701	ADA00707	ADA00700	ADA27292	ADA27291	ADA00703	ADA27294	ADS20227
				Ad139155	Adi39157	Abg74880	Abg74882	Abg74881	Ads20255	Ads20230	Adp87577	Adb85492	Aae38369	Ads20251	Adp18461	Ada00701	Ada00707	Ada 00700	Ada27292	Ada27291	Ada00703	Ada27294	Ads20227
				Construct			Bacteriop	Bacteriop	Human agg	Human agg	Human NOV	Human agg	Human agg	Human agg	Arthrobac	Modified	Modified	Modified	Plasmid p	Plasmid p	Modified	Plasmid p	Human agg

#### Streptavidin binding peptide SEQ ID NO 02-OCT-2002. Synthetic Streptavidin; DE10113776-A1 Misc-difference protein chip; microtitre plate; detection. Location/Qualifiers 9. .16 /label= unknown

21-MAR-2001; 2001DE-01013776.

21-MAR-2001;

2001DE-01013776

(BIOA-) INST BIOANALYTIK GMBH GOETTINGEN.

WPI; 2003-031166/03.

New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding modules.

Disclosure; Page 4; 18pp; German.

The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (PP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily

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Sequence 24

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controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention

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RESULT 2
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                     The invention relates to an isolated peptide (I) comprising at least two conditions in the contain and individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro:X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for urification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
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                                                                                                                                                                                                                                                                                                 protein, modules.
                                                                                                                                                                                                                                                              Claim 7; Page 16; 18pp; German
                                                                                                                                                                                                                                                                                                           New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding
                                                                                                                                                                                                                                                                                                                                                                                           Schmidt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP60369 standard;
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ilarity 100.0%;
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Pred. No. 2.1e-07;
Mismatches 0;
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Query Match

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WSHPQFEKGGGSGGGSGGGSGGGSWSHPQFEK

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Sequence

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Matches 16
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                                                                                                      The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein as [PP], also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                                                                                                                                                                                                                                                                                                                                                 protein, modules.
                                                                                  Sequence 36
                                                                                                                                                                                                                                                                                                                   Claim 8; Page 16; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                           New isolated peptide, useful as protein, comprises at least two
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                                          Local Similarity
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28"
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                           Score 94; DB
Pred. No. 5.3e
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           affinity purification tag for recombinant high-affinity streptavidin-binding
                      DB 6;
5.3e-05;
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contaminated any once of the first industrial for the heavy metal ions contaminated appears in the formation is useful for recombinantly comprising a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing comprision in the cell and culturing comprision for the produce a recombinant host cell and culturing comprision for the produce a recombinant host cell and culturing comprision for the cell and culturing divisions are contaminated soil, ground water, hydroponic solutions or irrigation composed to support, is useful for concentrating heavy metal ions from contaminated active in the first concentrating heavy metal ions from contaminated active including biological fluids. The nucleic acid, when recombinantly contaminated active in the invivo sequestration and elimination of contaminate for use in the invivo sequestration and elimination of contaxitable for use in the invivo sequestration and elimination of the invention are also useful in water treatment resins. The molecules of the contaxitable for useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as contaxitable for the invention such as collection (Auty7553-Auty7560) of synthetic contamination of the heavy metal binding proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons of the invention.
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids.
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001; 2001WO-US031819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   irrigation water; waste stream; contaminated aqueous medium;
biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic cadmium/mercury ion binding chelon protein
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    Local Similarity hes 9; Conserv
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Query Match

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Length 117;

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                                                                                          The present invention relates to a new non-naturally occurring CC recombinant DNA molecule comprising a sequence encoding a chelon protein CC which binds mercuric ions. The invention is useful for recombinantly CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a protein to produce a recombinant host cell and culturing CC region for the protein to produce a recombinant host cell and culturing CC mucleic acid encoding the chelon protein is useful for binding divalent CC mucleic acid encoding the chelon protein is useful for binding divalent CC mercuric ions, to take up, sequester and concentrate the heavy metal ions CC from contaminated soil, ground water, hydroponic solutions or irrigation CC water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal ions from CC contaminated environment waste streams or contaminated aqueous medium CC including biological fluids. The nucleic acid, when recombinantly capressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of CC coxic mercuric ion from gastrointestinal tracts of animals or humans exposed to coxic metal ions such as mercury and/or cadmium. The molecules of the coxic mercury or cadmium with high affinity. The present amino acid sequence cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins for the invention. This is requested to invention.
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biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
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CC which binds mercuric lons. The invention is useful for recombinantly
CC which binds mercuric lons. The invention is useful for recombinantly
CC producing a protein in a host-cell, by infecting or transforming a host
CC cell capable of expressing a chelon coding sequence with a vector
CC comprising a promoter active in the host cell operably linked to a coding
CC the recombinant host cell under conditions, where DNA is expressed. The
CC nucleic acidjencoding the chelon protein is useful for binding divalent
CC mercuric ions, to take up, sequester and concentrate the heavy metal ions
CC from contaminated soil, ground water, hydroponic solutions or irrigation
CC water of waste streams. The DNA of the invention, when immobilised onto a
CC solid support, is useful for concentrating heavy metal ions from
CC contaminated environment waste streams or contaminated aqueous medium
CC contaminated environment waste streams or contaminated aqueous medium
CC is suitable for use in the in vivo sequestration and elimination of
CC mercuric ions from gastrointestinal tracts of animals or humans exposed to
CC toxic metal ions such as mercury and/or cadmium. The molecules of the
CC invention are also useful in water treatment resins. The nucleic acid of
CC the invention is highly specific and binds divalent cation such as
CC mercury or cadmium with high affinity. The present amino acid sequence
CC cadmium/mercury ion binding chelon proteins of the invention. This
CC sequence is one of the heavy metal binding proteins termed chelons of the
invention.
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AAU97557
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cc producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent centruic ions, to take up, sequester and concentrate the heavy metal ions cfrom contaminated soil, ground water, hydroponic solutions or irrigation contaminated soil, ground water, hydroponic solutions or irrigation contaminated environment waste streams or contaminated apueous medium contaminated environment waste streams or contaminated apueous medium contaminated environment waste streams or contaminated aqueous medium contaminated environment waste streams or contaminated aqueous medium contaminated environment waste streams or contaminated aqueous medium contaminated environment waste streams or contaminated aqueous medium contaminated environment waste streams or contaminated aqueous medium contaminated environment waste streams or contaminated aqueous medium contaminated environment waste streams or contaminated apueous medium contaminated environment waste streams or contaminated action of the invention are also useful in water treatment resins. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury in bindies of the invention and elimination of specific and binds divalent cation such as mercury in bindies cholen specific and binds divalent cation such as
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biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
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cadmium/mercury ion binding chelon proteins

invention.

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The present invention relates to a new non-naturally occurring CC recombinant DNA molecule comprising a sequence encoding a chelon protein CC which binds mercuric ions. The invention is useful for recombinantly CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing CC the recombinant host cell under conditions, where DNA is expressed. The CC mercuric ions, to take up, sequester and concentrate the heavy metal ions CC from contaminated soil, ground water, hydroponic solutions or irrigation CC water of waste streams. The DNA of the invention, when immobilised onto a soild support, is useful for concentrating heavy metal ions from CC contaminated environment waste streams or contaminated aqueous medium CC including biological fluids. The pucleic acid, when recombinantly CC expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of concentrate ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as
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which binds mercuric ions. The invention is useful for recombinantly comparison of the producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The cultication contaminated soil, ground water, hydroponic solutions or irrigation contaminated soil, ground water, hydroponic solutions or irrigation contaminated environment waste streams or contaminated aqueous medial for contaminated environment waste streams or contaminated aqueous medial contaminated environment waste streams or contaminated aqueous medial conto a contaminated environment waste streams or contaminated aqueous medial conto including biological fluids. The nucleic acid, when recombinantly contaminated for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to
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                                                                                                                                                                                                                                                                                                                                                                                                 Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids.
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enteric bacteria; toxic metal ion; mercury;
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biological fluid;
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gastrointestinal tract; chelon
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                            The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal ions from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; Merk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (ANU9753-ANU97560) of synthetic cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids.
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environment waste streams or

contaminated

aqueous medium

The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation

Claim 4; Page

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English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                       Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids.
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52.9%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The
                                                                                                                                                                                                                                                                                                                     Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                  Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       irrigation water; waste stream; contaminated aqueous medium;
biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipocalin; anticalin; peptide loop; leaflet structure; antibody; therapy; tissue-specific surface molecule; tumour-specific surface molecule; tumour imaging; bilin binding protein; DsbC protein.
            Disclosure; Page 70-72; 80pp; German
                                         New anticalins produced by mutation of lipocalin family protein.
                                                                                                                                                                                                                                                                WO9916873-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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N-PSDB; AAX24100.
                                                                                                               Skerra A,
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                                                                                                               Beste G,
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                                                                                                                                                                                                                                                                                        /label= fusion_peptide
/note= "This fusion peptide is constructed from bilin
binding protein and a strep-Tag II region."
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RESULT 14
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Anticalins can bind to a predetermined ligand with determinable affinity. Anticalins of fusions of anticalins, are used: (a) when immobilized, for capture of the conjugates of the conjugation of ligands (or their conjugates). Typically they bind to tissue- or tumor-specific fusions or conjugates). Typically they bind to tissue- or tumor-specific surface molecules and can be used for tumour imaging or directly for conjugates of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugation of the conjugati
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DB; AAX24101.
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albumin binding domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                             Anticalins can bind to a predetermined ligand with determinable affinity. Anticalins or fusions of anticalins, are used: (a) when immobilized, for Anticalins or fusions of anticalins, are used: (a) when immobilized, for Separation; and (b) when labeled, for identification of ligands (or their fusions or conjugates). Typically they bind to tissue- or tumor-specific surface molecules and can be used for tumour imaging or directly for surface molecules and can be introduced into lipocalin polypeptides tumour therapy. Mutations can be introduced into lipocalin polypeptides more easily than into antibodies, since lipocalin polypeptides have only acid changes without significant effect on folding. Anticalins have high specific affinity, comparable with that for antibodies. This sequence specific affinity, comparable with that for antibodies. This sequence represents a fusion polypeptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the preparation of anticalins from polypeptides of the lipocalin family by mutation of amino acids in the region of the peptide loops (at one end of the cylindrical 'leaflet' structure).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New anticalins produced by mutation of lipocalin family protein.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 254 AA;
Bilin binding-protein associated protein #2.
                                                                                                                        AAB46421 standard; protein; 254
                                           06-APR-2001
                                                                                     AAB46421
                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                           l Similarity
9; Conserva
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                                              (first entry)
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                                                                                                                                                                                                                                                                                                                 Score 63; DB pred. No. 11; 8; Mismatches
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Bilin-binding protein; mutein; BBP; digoxigenin.
This invention describes novel polypeptides (I) that are muteins of bilin -binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-mainofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88, 90, 95, 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low
                                                                                                                                                   New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for digoxigenin.
                                                                                                                                                                                                          WPI; 2001-071071/08.
N-PSDB; AAF25703.
                                                                                                                                                                                                                                                                                                                                08-JUN-2000; 2000WO-DE001873
                                                                                                                                                                                                                                                                                                                                                            14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                       WO200075308-A1
                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                  Skerra A,
                                                                                                                                                                                                                                                                                                        08-JUN-1999;
                                                                                                                          Example 1; Page 59-60; 80pp; German
                                                                                                                                                                                                                                                                            (SKER/) SKERRA A.
                                                                                                                                                                                                                                                    Schlehuber S;
                                                                                                                                                                                                                                                                                                         99DE-01026068
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CC used as a label. Compared with Dig-specific antibodies, (I) have a cc simpler structure and are easier to prepare. They have very high cc specificity for Dig, relative to other steroids, and fusion partners may be attached to either end without compromising their ability to bind cc ligand cc ligand system to state the compromising their ability to bind compromise the compared compromise of the compared compromise of the compared compromise of the compared compromise of the compared compromise of the compared compromise of the compared compared compromise of the compared compared compromise of the compared compared compromise of the compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared compared
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                         Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

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105.489 Million cell updates/sec
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SUMMARIES
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Sequence 3, Appli Sequence 10, Appl Sequence 11, Appl Sequence 30, Appl Sequence 33, Appl Sequence 4, Appli Sequence 7, Appli Sequence 7, Appli Sequence 8, Appli Sequence 9, Appli Sequence 10, Appl Sequence 11, Appl Sequence 11, Appl	Description

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# ALIGNMENTS

US-10-026-578B-3

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Sequence 3, Application US/10026578B

Publication No. US20030083474A1

GENERAL INFORMATION:

APPLICANT: SEA (GmbH)

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APPLICANT: SEA (GmbH)

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APPLICANT: SEA (GmbH)

APPLICANTON UNDER: US/10/026,578B

CURRENT APPLICATION UNDER: US/10/026,578B

CURRENT APPLICATION UNDER: US/10/026,578B

CURRENT APPLICATION UNDER: DOI: 10.1

PRIOR APPLICATION UNDER: DOI: 10.1

PRIOR APPLICATION UNDER: DOI: 10.1

ANMERE: POT/EPO1/11846

PRIOR FILING DATE: 2001-0-12

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PATELING DATE: 2001-10-12

SOFTWARE: PATELING DATE: 2001-10-12

SOFTWARE: PATELING DATE: 2001-10-12

SOFTWARE: PATELING DATE: 2001-10-12

SOFTWARE: PATELING DATE: 2001-10-12

SOFTWARE: PATELING DATE: 2001-10-12

SOFTWARE: NISC FEATURE

LOCATION: (10) ... (10)

OTHER INFORMATION: X represents a single amino acid at the position indicated FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (10) ... (10)

OTHER INFORMATION: X represents a single amino acid at the position indicated FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (11) ... (11)

OTHER INFORMATION: X represents a single amino acid at the position indicated FEATURE:

NAME/KEY: MISC FEATURE

LOCATION: (11) ... (11)

OTHER INFORMATION: X represents a single amino acid at the position indicated FEATURE:

NAME/KEY: MISC FEATURE

NAME/KEY: MISC FEATURE

LOCATION: (11) ... (11)

OTHER INFORMATION: X represents a single amino acid at the position indicated FEATURE:

PRIOR APPLICATION: (11) ... (11)

PRIOR METERICANTION: X represents a single amino acid at the position indicated FEATURE INFORMATION: X represents a single amino acid at the position indicated FEATURE INFORMATION: X represents a single amino acid at the position indicated FEATURE INFORMATION: X represents a single amino acid at the position indicated PATELING INFORMATION: X represents a single amino acid at the position indicated
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                                                                                                                               ; NAME/KEY: misc_feature
; OTHER INFORMATION: Artificial Sequence represents peptide binding module
US-10-026-578B-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10026578B

Publication No. US20030083474A1

GENERAL INFORMATION:

APPLICANT: IBA (GmbH)

APPLICANT: Schmidt, Thomas

TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta

FILE REFERENCE: 100810.01US1

CURRENT APPLICATION NUMBER: US/10/026,578B

CURRENT FILING DATE: 2002-11-11

PRIOR APPLICATION NUMBER: DE 101 13 776.1

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: PCT/EP01/11846

PRIOR FILING DATE: 2001-10-12

NUMBER: DOT NOS-14
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                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATION: Artificial Sequence represents
                                                                                                                                                                                                 OTHER INFORMATION: Missing, the total numbers of x will be no less than 5 OTHER INFORMATION: missing, the total numbers of x will be no less than 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (12)^{\top}. (12)
OTHER INFORMATION: X represents a single amino acid at the position indicated
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                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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OTHER INFORMATION: X represents a single amino
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                                                                                                                                                                                                                                                              LOCATION: (9)
                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 36
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-XXXXXXXXWSHPQFEK 24
                                                                        Score 94; DB 14;
Pred. No. 0.00012;
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Pred. No. 6.3e-07;
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US-10-026-578B-11
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                                                                  US-09-809-517A-30
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                                                                                                                                                                                                                                                            Sequence 30, Application US/09809517A
Patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR PRILING DATE: 1999-07-20
PRIOR PRILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
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Best Local
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TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR PILING DATE: 2001-03-21
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APPLICANT: Schmidt,
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 41
                                                                                                                                                   LENGTH: 21
TYPE: PRT
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OTHER INFORMATION: be present
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OTHER INFORMATION: Cof the five
OTHER INFORMATION: repeats may
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                                                                                       OTHER INFORMATION: Description of Artificial Sequence: synthetic module
                                                                                                              FEATURE:
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58.2%;
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Pred. No. 0.0058;
B; Mismatches
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  No.
    DB 9;
0.49;
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Query Match Best Local Similarity

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PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patcentin version 3.0
SEQ ID NO 33
LENGTH: 22
Type: nome
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US-09-809-517A-33
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                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 117
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Matches 9; Conserv
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Best Local
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TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Summers, Anne O.
APPLICANT: Caguist, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                          ORGANISM: Artificial Sequence
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ORGANISM: artificial sequence
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KGNVSCPSAWSHPQFEK 117
                                KDDDDKGAPWSHPQFEK 21
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                                                                                     Score 64; Pred. No. 3
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PRIOR APPLICATION NUMBER: 2001-10-12
PRIOR FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 117
TYPE: TYPE: 117
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Publication No. US20030104524A1
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
                                                       Query Match
Best Local Similarity 52.9
Conservative
                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7
LENGTH: 117
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Best Local
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Metal Binding Proteins, TITLE OF INVENTION: Methods
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TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
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CURRENT FILING DATE: 2001-10-12
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                             TYPE: PRT
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101 KGNVSCPSAWSHPQFEK 117
                  8 KXXXXXXXXXWSHPQFEK 24
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52.9%; Pred. No. 3
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Pred. No.
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RESULT 9 US-09-977-137A-8

Sequence 8, Application US/09977137A Publication No. US20030104524A1 GENERAL INFORMATION:
APPLICANT: Summers, Anne O.

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US-09-977-137A-10
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                                                                                                                                                               Sequence 10, Application US/09977137A Publication No. US20030104524A1
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SEQ ID NO 9
LENGTH: 117
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 117
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                                                     APPLICANT: Summers, Anne O.
APPLICANT: Cagulat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OP INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OP INVENTION: Methods
FILE REFERENCE: 79-00
                 CURRENT APPLICATION NUMBER: US/09/977,137A CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
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nes 9; Conserv
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NUMBER: US 60/240,465
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Pred. No. 3.7;
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APPLICANT: Summers, Anne O.
APPLICANT: Cagulat, Jonathan
ITILE OF INVENTION: Metal Binding Proteins, Re
ITILE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
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US-09-977-137A-12
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; TITLE OF INVENTION: Metal Binding Proteins, Re
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 79-00
; CURRENT APPLICATION NUMBER: US/09/977,137A
; CURRENT FILLING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,465
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 18
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US-09-977-137A-11
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NUMBER OF SEQ ID NOS: 18
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ORGANISM: Artificial Sequence
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Sequence 40, Application US/10628432

| Publication No. US20040142863A1
| GENERAL INFORMATION:
| APPLICANT: Wyeth
| TITLE OF INVENTION: Modified ADAMTS4 molecules
| FILE REFERENCE: AM101378
| CURRENT APPLICATION NUMBER: US/10/628,432
| CURRENT FILING DATE: 2003-07-29
| NUMBER OF SEQ ID NOS: 53
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 40
| LENGTH: 845
| TYPE: PRT
| ORGANISM: Artificial
| OTHER INFORMATION: ADAMTS4 ASM with insertion
| US-10-628-432-40
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and

TITLE OF INVENTION: Methods

FILE REFERENCE: 79-00

CURRENT APPLICATION NUMBER: US/09/977,137A

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 60/240,465

PRIOR TILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin ver. 2.0

SEQ ID NO 6

LENGTH: 118

TYPE: PAT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: chelon
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                                                                            Query Match 56.4%; Score 62; DB 16; Length 845; Best Local Similarity 44.4%; Pred. No. 67; Matches 8; Conservative 10; Mismatches 0; Indels
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Best Local Similarity
Matches 9; Conserv
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102 KGNVSCPSAWSHPQFEK 118
                             7 EXXXXXXXXXSHPQFEK 24
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                                   Score
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  protein search, using
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-09-382-7368-8
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50	50	50	50	50	50	50	50	50	50	50	51	51	51	51	51	51	51
45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	45.5	46.4	46.4	46.4	46.4	46.4	46.4	46.4
867	771	645	574	. 527	527	527	487	356	273	158	537	476	420	406	204	108	94
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US-09-547-435-24	US-09-547-435-28	US-09-547-435-26	US-09-438-185A-489	US-09-600-985-3	US-09-600-985-2	US-09-600-985-1	US-09-602-777A-420	US-09-198-452A-526	US-09-328-352-6417	US-09-621-976-4227	US-09-949-016-5954	US-09-949-016-10314	US-09-949-016-9364	US-09-248-796A-16826	US-09-248-796A-16426	US-09-023-905A-32	US-09-438-185A-640
Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
24, Appl	28, Appl	26, Appl	489, App	3, Appli	<ol><li>Appli</li></ol>	1, Appli	420, App	526, App	6417, Ap	4227, Ap	5954, Ap	10314, A	9364, Ap	16826, A	16426, A	32, Appl	640, App

### ALIGNMENTS

US-09-809-517A-30

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RESULT 2
US-09-809-517A-33
; Sequence 33, Application US/09809517A
; Sequence 33, Application US/09809517A
; Patent No. 6753136
; GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. 6753136el methods for displaying (poly) peptides/proteins on TITLE OF INVENTION: particles via disulfide bonds
; TITLE OF INVENTION: particles via disulfide bonds
; FILE REFERENCE: MORPHO/11
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR APPLICATION NUMBER: EP 99114072.4
; PRIOR APPLICATION UNMBER: EP 00103551.8
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 41
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                                                                                       SEQ ID NO 5
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Patent No. 675004
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Patent No. 6750042
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                                                                                                                               CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                 APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                       NUMBER OF SEQ ID NOS: 18
                                                                                                     SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
                                 TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
OTHER INFORMATION: Description of Artificial Sequence:
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                                                                       ENGTH: 117
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Pred. No. 0.028;
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                                                                   ; OTHER INFORMATION: Description of Artificial Sequence: chelon US-09-977-137A-8
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      Matches
                  Query Match
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APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonath
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Patent No. 6750042
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Patent No. 6750042
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                                                                                                                                                                              NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                            APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                  FILE REFERENCE: 79-00
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                                                                                                              LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
FEATURE:
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Pred. No.
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Pred. No. 0.28;
   Mismatches
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FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 10
SEQ ID NO 10
LENGTH: 117
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
RESULT 9
US-09-977-137A-11
; Sequence 11, Application US/09977137A
                                                                                                                                                                                                                 ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: chelon US-09-977-137A-10
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US-09-977-137A-9
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US-09-977-137A-9
                                                                                                                                                    Query Match
Best Local Similarity
Matches 9; Conserv
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sudmers, Anne O.
APPLICANT: Cagulat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/240,465 PRIOR FILING DATE: 2000-10-12
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Artificial Sequence
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KGNVSCPSAWSHPQFEK 117
                                                                                     KGNVSCPSAWSHPQFEK 117
                                                                                                                                                       Conservative
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Pred. No. (
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION UNMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 117
TYPE: PRT
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; OTHER INFORMATION: Description of Artificial Sequence: chelon US-09-977-137A-12
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US-09-977-137A-6
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APPLICANT: Cagulat, Jonathan
APPLICANT: Cagulat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Re
TITLE OF INVENTION: Methods
FILL REPERENCE: 79-00
CURRENT APPLICATION UNMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: US-09-977-137A-11
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Best Local Similarity 52.>
"Chee 9; Conservative
                                                   Sequence 6, Application US/09977137A
Patent No. 6750042
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
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LENGTH: 117
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Best Local Similarity
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                    Sequence 34, Application US/09809517A
Patent No. 6753136
GENERAL INFORMATION:
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SEQ ID NO 31
LENGTH: 24
TYPE: PRT
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly) peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR PILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR PILING DATE: 2000-02-18
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Best Local &
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APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
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Best Local .
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CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
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NUMBER OF SEQ ID NOS: 41
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
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PRIOR FILING DATE: 1999-07-20
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SOFTWARE: PatentIn Ver. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: synthetic module
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Pred. No. 0.
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Pred. No. 0.29;
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US-09-732-210-1454
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                                                                                                                                                           APPLICANT: Bunkers, ()
APPLICANT: Liang, J;
APPLICANT: Mittanck,
APPLICANT: Seale, J;
APPLICANT: Wu, Yonni
                                                                                                                                                                                                                                                     Sequence 1454, Appli
Patent No. 6573361
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SEQ ID NO 995
LENGTH: 699
TYPE: PRT
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SEQ ID NO 34
LENGTH: 25
TYPE: PRT
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT FILING TON NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: 60/127,352
PRIOR PILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
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Best Local Similarity
               PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
                                                                                APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and FILE REFERENCE: 38-21 (15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
TUMBER OF SEQ ID NOS: 1753
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Mittanck, Cindy A.
Seale, Jeffrey W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB
Pred. No. 67;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 61; DB
Pred. No. 0.09
10; Mismatches
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0.091;
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Page 5
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Search completed: March 2, 2005, 12:25:37 Job time : 28.3171 secs ; SEQ ID NO 1454 ; LENGTH: 83 ; TYPE: PRT ; ORCANISM: Chlamydia trachomatis US-09-732-210-1454 Query Match 49.1%; Score 54; DB 4; Length 83; Best Local Similarity 26.1%; Pred. No. 4.9; Matches 6; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

음 성

This Pogo Blonk (USOYO)

1

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
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March 2, 2005, 12:20:44; Search time 19:1057 Seconds (without alignments)
125:901 Million cell updates/sec

Title: SEQ13
Perfect score: 111
Sequence: 1 wshpqfe

Run on:

quence: 1 wshpqfekxxxxxxxxxxxxxxshpqfek 25

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR 79:\*
pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	თ	5.	4	w	N	٦	Result No.
52	52	52	52	52	52	'n	52.5			53	54	54	54	54	54	54	54	55						55		56	57	58	Score
46.8	46.8	6	•	٥.	•	47.3	47.3	47.7	47.7	47.7	48.6	48.6	48.6	48.6	48.6	8	B	49.5	49.5	49.5	9	49.5	49.5	49.5	49.5	50.5	۲	52.3	Query
633	451	434	323	226	108	699	220	437	83	83	2150	2150	958	625	414	308	260	379	330	318	315	103	103	103	103	759	73	1113	Length
Ν	N	N	N	N	N	N	ب	N	N	۲	N	ب	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	BB
D72284	012	G95297	E88642	E83081	F95385	A54660	S22516	A31142	F81664	C42645	T19450	S27802	862413	G72420	G84311	G86464	AB2080	T23592	AC2071	S76226	T23597	A90904	C85713	A85821	E90973	D81657	S28978	T20004	ID
oligopeptide ABC t	recepin - human	probable hydrolase	protein C54E4.5 [i	գ	protein [imported	histidine rich cal	S-allele-associate	gelsolin, ovarian		ribosomal protein	cal	prote	probable sulfate t	ABC	hypothetical prote			_	ical	_	ical	hypothetical prote	unknown protein en		hypothetical prote	etion	erb protein - phag	o	Description

A;Gene: srb A;Start codon: GTG

Query Match 51.4%; Score 57; DB 2; Length 73; Best Local Similarity 36.4%; Pred. No. 2.1; Matches 8; Conservative 11; Mismatches 3; Indels

0,

Gaps

0

45	44	43	42	41	40	39	38	37	36	35	34	<u>υ</u>	32	31	30
50	50	50	50.5	51	51	51	51	51	51	51	51	51	51.5	52	52
45.0	45.0	45.0	45.5	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	45.9	46.4	46.8	46.8
161	86	86	1078	3947	1003	754	754	664	656	318	. 225	109	71	957	760
N	N	N	N	N	N	N	N	N	N	N	N	N	_	N	2
B42627	H72054	C86570	877162	T52486	T28654	D72032	E86592	A47012	T01573	B75382	A75425	E89873	IHER1	T10633	E71499
cement precursor p	ribosomal protein	S17 ribosomal prot	DNA topoisomerase	ferrichrome sidero	transposase - Pseu	general secretion	general secretion	phenol 2-monooxyge	earl protein - mai	conserved hypothet	hypothetical prote	cysteine protieina	high potential iro	hypothetical prote	probable gen. secr

## ALIGNMENTS

RESULT 2 \$28978 \$28978 \$28978 \$28978 \$28978 G;Species: phage HK022 G;Species: phage HK022 G;Pate: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004 G;Accession: \$28978; \$16858 R;Atkinson, B.L.; Gottesman, M.E. J. Mol. Biol. 227, 29-37, 1992 A;Title: The Escherichia coli rpoB60 mutation blocks antitermination by coliphage HK022 A;Reference number: \$28977; MUID:92395669; PMID:1522593 A;Accession: \$28978 A;Molecule type: DNA A;Residues: 1-73 <atk> A;Cross-references: UNIPROT:Q38575; EMBL:X60308; NID:g15753; PIDN:CAA42853.1; PID:g57915 C;Genetics:</atk>	A; Map Dosition: 4 A; Map Dosition: 4 A; Map Dosition: 65/3; 112/2; 213/3; 574/3; 968/3; 1070/2 C; Superfamily: ubiquitin-activating enzyme E1 Query Match 52.3%; Score 58; DB 2; Length 1113; Best Local Similarity 34.8%; Pred. No. 37; Matches 8; Conservative 11; Mismatches 4; Indels 0; Gaps 0; Qy 2 SHPQPEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	RESULT 1  T20004  hypothetical protein C47E12.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T20004 R;Coles L. submitted to the EMBL Data Library, January 1996 A;Reference number: Z19210 A;Accession: T20004 A;Accession: T20004 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rolecule type: DNA A;Rolecule type: DNA A;Residues: 1-1113 <wil> A;Experimental source: clone C47E12 C;Genee (GESP-C47E12, 5</wil>
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E90973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein ECs2757 [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (c;Species: Bscherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: E90973
    A;Title:
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A;Molecule type: DNA
A;Residues: 1-759 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber Nucleic Acids Res. 28, 1397-1406, 2000. A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q8X4V0; GB:BA000007; PIDN:BAB36180.1; PID:g13362225; GSPDB
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-103 < HAY>
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A;Experimental source: strain Nigg
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        Genome
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6; Conserv
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  sequence of enterohemorrhagic Escherichia coli 0157:H7
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Pred. No.
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                                      Matches
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C;Species: Escherichia coli
C;Date: 10-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A99004
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, T.; Kuhara, S.; Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, Shiba, 
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                                                                                                                                A;Cross-references: UNIPROT:Q8X549; GB:BA000007; PIDN:BAB35624.1; A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia
A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Residues: 1-103 <STO>
A;Cross-references: UNIPROT:Q8X4V0; GB:AE005174; NID:g12516136; PIDN:AAG57029.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain ED1933
                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-103 < HAY>
                                                                                                                                                                                                                                                                                                    A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ECs2201 [imported] -
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A; Residues: 1-103 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: C85713
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown protein encoded within prophage CP-9330 [imported] - Escherichia coli (strain
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Score 55;
Pred. No.
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Pred. No.
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EDL933
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Potamousis,
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C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 12-Jul-2004 C;Accession: S76226 C;Accession: S76226 R;Xaneko, T.; Sado, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996 DNA Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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A;Introns: 18/3; 105/2; 143/1; 231/2
C:Superfamily: ribitol dehydrogenase:
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                                    hypothetical protein all2121 [imported] - Nostoc sp. (strain PCC 7120) C;Species: Nostoc sp. PCC 7120 C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 12-Jul-2004
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A;Note: the nucleotide sequence was submitted to C;Superfamily: 24-sterol C-methyltransferase F;94-195/Domain: bioC homology <BIOC>
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C;Species: Synechoc
A;Variety: PCC 6803
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A, Accession: S76226
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A; Residues: 1-315 <WIL>
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;Accession: AC2071
;Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
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38.9%;
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25.0%; Pred. No.
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Pred. No.
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change (C;Accession: AB2080
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M. DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fi
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A;Residues: 1-330 <KUR>
A;Cross-references: UNIPROT:Q8YV60; GB:BA000019;
A;Cross-references: strain PCC 7120
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A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AC2071
A; Experimental source: strain PCC C; Genetics:
                                    A;Molecule type: DNA
A;Residues: 1-260 <KUR>
A;Cross-references: UNIPROT:Q8YUY9; GB:BA000019;
                                                                                                  A; Status: preliminary
                                                                                                                     A;Reference number: AB1807;
A;Accession: AB2080
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A;Introns: 76/3; 163/2; 199/3; 295/2
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C; Superfamily: 24-sterol C-methyltransferase
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                                                                                                                                                                                                                                                                                                                              hypothetical protein all2192 [imported] - Nostoc sp.
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NA Res. 8, 205-213, 2001
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                                                                                                                                             Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840
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25.0%; Pred. No.
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C;ACCESSION: G86464
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, R;Theologis, A.; Ecker, J.R.; Conmay, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Ching, M.K.; Conm., L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

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ansen, N.F.; Hughes, B.; Huizar, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

A;Authors: Hunter, J.L.; Liu, S.K.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.K.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.K.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marziali, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.K.; Liuros, J.S.; Southwick, A.M.; Sun, H.; Tallon, Rizzo, M.; Rooney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.W.; Venter, J.C.; Davis, R.W.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Paris, S.R.; R.W.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Paris, S.R.; Schwartz, J.R.; Paris, S.R.; Schwartz, J.R.; Paris, S.R.; Schwartz, J.R.; Paris, S.R.; Schwartz, J.R.; Paris, S.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwartz, J.R.; Schwar
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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A; Molecule type: DNA
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proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.

A;Title: Genome sequence of Halbbacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: G84311
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A;Gene: VNG1585C
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A; Residues: 1-414 <STO>
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, Apacession: Kennedy, S.D.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
, Ng, W.V.; Kennedy, S.D.; Mahairas, G.G.; Berquist, B.; Pan, M.; Maddocks, D.C.
Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.C.
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RESULT 15
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A;Molecule type: DNA
A;Residuse: 1-625 <ARN>
A;Cross-references: UNIPROT:Q9WXS6; GB:AE001694; GB:AE000512; NID:g4980558; PIDN:AAD3516
A;Cross-references: UNIPROT:Q9WXS6; GB:AE001694; GB:AE000512; NID:g4980558; PIDN:AAD3516
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A;Gene: TM0071
C;Superfamily: dipeptide transport protein
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A;Tittle: Evidence for lateral gene transfer between Archaea and Bacteria from genome sequa, Reference number: A72200; MUID:99287316; PMID:10360571
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Search completed: March Job time : 20.1057 secs
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270 AA. ence update) tation update) ; Trypanosomatidae		; DB 2; Length 74 1. 16; tches 1; Indels	2; 1. 3E0982813A CRC64	•	ling cascade; IEA	IEA.	/GenBank/DDBJ databas	/ertebrata;   ni; Muridae;	ence update) tation update) nit E219G mutant	743 AA.	ENTS		
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REMBL; AJ316576; CAC87723.1; -.

RO; GO:0004177; F:aminopeptidase activity; IEA.

RO; GO:0003924; F:catalytic activity; IEA.

R InterPro; IPR00326; Lipase AS.

R InterPro; IPR003775; Peptidase S9.

R InterPro; IPR000379; Ser estrs.

DR InterPro; IPR000897; SRP54.

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DR PROSITE; PS00300; SRP54; UNKNOWN_1.

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DOI=10.1128/AEM.59.2.1246-1250.2003;
Basten D.E.J.W., Dekker P.J.T., Schaap
"Aminopeptidase C of Aspergillus niger
aminopeptidase.";
                                                                                                                                                                                      Aminopeptidase.
SEQUENCE 663
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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SEQUENCE 270 AA; 29661 MW; 60829CD354CFBB36 CF
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MEDLINE=98146435;
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Best Local
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GO; GO:0005514; F:calcium ion storage activity; IEGO; GO:0051082; F:unfolded protein binding; IEA.
GO; GO:005487; P:protein folding; IEA.
InterPro; IPR001580; Calret/calnex.
InterPro; IPR001580; Calret(culin.
InterPro; IPR009139; Calret culin.
InterPro; IPR009033; Calret culins.
InterPro; IPR009085; Contactivation;
InterPro; IPR008085; Contactivation;
InterPro; IPR008086; R target S.
Pfam; PF00262; Calretivatin; I.
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01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2004 (TrEMBLrel. 26, L
Calreticulin precursor.
Name-calret;
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01-MAY-2000
01-MAY-2000
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: Belongs to the calreticulin fa
EMBL; AF177915; AAD55725.1; --
HSSP; P18418; IKCC.
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
Strongylocentrotus.
PIRSF; PIRSF002356; Calreticulin; 1.
PRINTS; PRO0626; CALRETICULIN.
PROSITE; PS00804; CALRETICULIN_REPEAT; 3.
PROSITE; PS00805; CALRETICULIN_REPEAT; 3.
PROSITE; PS00014; ER TARGET; UNKNOWN 1.
Chapperone; Endoplasmic reticulum; Signal.
Chapperone; 19
Potential.
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OrderedLocusNames=Bd2365;
Bdellovibrio bacteriovorus.
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Science 303:689-692(2004).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB
PubMed=14752164; DOI=10.1126/Bcience.1093027;
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Nakamura I., Suzuki N.;

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databas

R EMBL; AB096020; BAC24016.1; -.

R HSSP; P30803; 1AZS.

R GO; GO:000433; F:guanylate cyclase activity; IEA.

R GO; GO:0016829; F:lyase activity; IEA.

R GO; GO:0007242; P:intracellular signaling cascade; I.

R GO; GO:0007242; P:intracellular signaling cascade; I.

Interpro; IPR001054; G_cyclase.

R Interpro; IPR001054; G_cyclase.

R Pfam; PF00211; Guanylate_cyc; 1.

R Pfam; PF00211; Guanylate_cyc; 1.

R PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.

R PROSITE; PS00452; GUANYLATE_CYCLASES_2; 1.
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Best Local S
Matches 8
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EQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C59BL/6J; TISSUE=Mammary gland;

MEDLINE=22388257; PubMede12477932; DOI=10.1073/pnas.242603899;

MEDLINE=22388257; PubMede12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Magner L., Shenmen C.M., Schuler G.D.

Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T
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Q8CJD2;
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SEQUENCE
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SEQUENCE
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                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                  Mus musculus (Mouse).
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01-MAR-2004 (TrEMBLrel.
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Mammalia; Eutheria; Rodentia;
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25, Last annotation
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Pred. No.
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.!
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk !
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.J
Jones S.J., Marra M.A.;
"Generatic Schein J.!"
"Generatic Schein J.!"
                                                                                                                                                                                                                                                                                                                       EMBL; Z68882; CAA93101.1;
PIR; T20004; T20004.
HSSP; Q8TBC4; 1NGV.
WormBase; WBGene00006699;
                                                                                                          WormPep; C47E12.5; CE05449.
G0; G0:0003824; F:catalytic activit G0; G0:0004839; F:ubiquitin activat G0; G0:0006512; P:ubiquitin cycle; InterPro; IPR009036; MoeB.
InterPro; IPR009036; NAD BS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q27481 PRELIMINARY; PRT; 1113 AA. Q27481; O1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypochetical protein C47E12.5. Name=uba-1; ORFNames=C47E12.5;
                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coles L.;
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Submitted (MAY-2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=6239;
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STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'Genome sequence of the nematode C.elegans: investigating biology.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Generation and initial analysis of more than 15,000
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; IPR009036; MOOB.
;; IPR0009205; NAD BS.
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l. Acad. Sci. U.S.A. 99:16899-16903(2002)
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; TISSUE=Mammary gland;
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                                                                                                                                                                                                                        activating
                                                                                                                                                                                                                                                                activity;
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Bouffard G.G.,
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vi-mar-2004 (TrEMBLrel. 26, Created)
01-Mar-2004 (TrEMBLrel. 26, Last sequence update)
01-Mar-2004 (TrEMBLrel. 26, Last annotation update)
2-polyprenyl-6-methoxyphenol hydroxylase.
Vibrio vulnificus (***)
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Pfam; PF02134; UBACT; 2.
PRINTS; PR01849; UBIQUITINACT.
PIGREMMS; TIGR01408; UBOL; 1.
PROSITE; PS00865; UBIQUITIN_ACTIVAT_2; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 1113 AA; 124083 MW; BD2198A97E4066CC CRC64;
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                         Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases. EMBL; X60308; CAA42853.1; -. EMBLJ, AF069308; AAF30374.1; -. PIR; S28978; S28978.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Juhala R., Ford M.E.,
                                                                                                                                                                                                                                                                                                                                                     "Genomic sequences of bacteriophages HK97 and mosaicism in the lambdoid bacteriophages."; J. Mol. Biol. 299:27-51(2000).
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Atkinson B.L., Gottesman M.E.;
"The E. coli rpoB60 mutation blocks antitermination by coliphage HK022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses,
Lambda-like viruses.
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05-JUL-2004
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mes 8; Conserv
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                                                                                                                                                                                                                                                                                                                  Youlton A.,
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Youlton A., Hatfull G.F.,
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                                                                                                                                                                                                           DB 2;
15;
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Matches 6
                                                                                                             "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; ABD16797; AAO08799.1; ---
REMBL; ABD16797; AAO08799.1; ---
REMBL; ABD16797; F.:nonooxygenase activity; IEA.
RGO; GO:0004497; F.:nonooxygenase activity; IEA.
RGO; GO:0006115; P:aromatic compound metabolism; IEA.
RGO; GO:0006115; P:alectron transport; IEA.
RGO; GO:0006115; P:alectron transport; IEA.
RINEETRO; IPR0010713; Flav monoxygenase.
RINEETRO; IPR010971; Ubi OHases.
RINEETRO; IPR010971; Ubi OHases; 1.
RPINTS; PR01420; RNGMNOXGNASE.
TICRFAMB; TICR01988; Ubi-OHases; 1.
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Q8DFE9 (TrEMBLrel 23,
Q1-MAR-2003 (TrEMBLrel 23,
Q1-MAR-2004 (TrEMBLrel 26,
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PubMed=14656965; DOI=10.1101/gr.1295503;

Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C., Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;

Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;

"Comparative genome analysis of Vibrio vulnificus, a marine
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Vibrionaceae; Vibrio.
NCBI_TaxID=196600;
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Complete proteome.
SEQUENCE 406 AA; 45816 MW; 20A7
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InterPro; IPR000205; NAD BS.
InterPro; IPR0003042; Rng_mnoxygenase.
InterPro; IPR0103042; Lbi_OHases.
Pfam; PF01360; Monooxygenase; 1.
PRINTS; PR00420; RNGMNOXGNASE.
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GO; GO:0004497; F:monooxygenase activity; IEA.
GO; GO:0006725; P:aromatic compound metabolism;
GO; GO:0006118; P:electron transport; IEA.
                                                                                                                                                                                                                                                                                                Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Choy H.E.;
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Vibrionaceae; Vibrio.
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Pred. No.
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MEDLINE-21637800; PubMed=11779357; DOI=10.1089/088922201753342103;

Mashishi T., Loubser S., Hide W., Hunt G., Morris L., Ramjee G.,

Abdool-Karim S., Williamson C., Gray C.M.;

"Conserved domains of subtype C nef from South African HIV type 1-
infected individuals include cytotoxic T lymphocyte epitope-rich
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mashishi T.N., Loubser S., Hide W., Hunt G., Morris L., Ramjee Abdool-Karim S., Williamson C., Gray C.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF397538; AAK58477.1; -.
HSSP, P04324; 1ZEC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY395247; AAR29933.1; -.
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Paraaitiformes; Ixodida; Ixodidae; Amblyomma.
NCBI_TaxID=257691;
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01-OCT-2002
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Pfam; PF00263; Secretin N; 2.
PRINTS; PR00311; BCTERIĀLGSPD.
PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
Complete proteome; Transport.
Complete proteome; 33771 MW; 7D5DDF55ED3FBA31
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Q9PUGB:
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
General secretion pathway protein D.
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SEQUENCE FROM N.A.

MEDLINE=22667917; PubMed=12781722;

Hardies S.C., Comeau A.M., Serwer P., Suttle C.A.;

"The complete sequence of marine bacteriophage VpV262 infecting vibrio parahaemolyticus indicates that an ancestral component of a T7 viral supergroup is widespread in the marine environment.";

Virology 310:359-371(2003).
                                                                                                                                                                                                                                                  Viruses, dsDNA v
T7-like viruses.
                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TYEMBLYE1. 22, Create 01-OCT-2002 (TYEMBLYE1. 22, Last a 01-OCT-2003 (TYEMBLYE1. 25, Last a 5' to 3' exonuclease-like protein.
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GO; GO:009306; P:protein secretion; I
InterPro; IPR001775; Bac GSPD.
InterPro; IPR001846; GSPII/IIIprotein.
InterPro; IPR001220; Lectin legB.
InterPro; IPR005644; NolW-like.
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Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae;
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                                                                                                                                                                                                                                                                                                                  Vibriophage VpV262
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-!- SIMILARITY: Belongs to the GSP D family.
EMBL; AE002352; AAF39657.1; -.
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ABP60369
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                          ADS20230
ADR70320
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ADR70386
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                                                                                                                            Ads20243 Human agg
Aaw93967 Plaamid p
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Ada27293
Ada00702
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Aab46420
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Abp60369 Streptavi
Abp60370 Streptavi
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Apolipopr
Plasmid p
Modified
Murine an
Human NOV
Human agg
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Polioviru
Polioviru
Polioviru
Polioviru
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Bilin bin
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ALIGNMENTS	AAU97555	AAU97559	AAU97557	AAU97553	AAU97558	ADS20227	AAU79048	ADS20249	ADR28055	AD025156	AD025151	AD025152	AD025150	AD025149	AD025155	ADO25154	ADO25153	ADO25157	ADS17525	ADR28054
	Aau97555 Synthetic	Aau97559 Synthetic	Aau97557 Synthetic	Aau97553 Synthetic	Aau97558 Synthetic	Ads20227 Human agg	Aau79048 Aspergill	Ads20249 Furin-pro	Adr28055 NPB polyp	Ado25156 Melanoma	Ado25151 Melanoma	Ado25152 Melanoma	Ado25150 Melanoma	Ado25149 Melanoma	Ado25155 Melanoma	Ado25154 Melanoma	Ado25153 Melanoma	Ado25157 Melanoma	Ads17525 Amino aci	Adr28054 NPB polyp
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#### RESULT 1 ABP60362 Streptavidin; protein chip; microtitre plate; detection. Streptavidin binding peptide 21-MAR-2001; 2001DE-01013776 02-OCT-2002. Misc-difference Synthetic 28-MAR-2003 ABP60362; ABP60362 standard; peptide; 21-MAR-2001; 2001DE-01013776. DE10113776-A1 (BIOA-) INST BIOANALYTIK GMBH GOETTINGEN. (first entry) Location/Qualifiers /label= unknown 24 SEQ ID ₿ ğ

The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily

eins (II) (so it and has easily

New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding modules.

WPI; 2003-031166/03.

Disclosure; Page 4; 18pp; German:

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RESULT 2
ABP60369
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Best Local S
Matches 24
                           The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein s (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin binding peptide SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
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                                                                                                                                                                                                                                                                                                                               New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding
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Sequence 35
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                                                                                                                                                                                                                                                                               Claim 7; Page 16; 18pp;
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Pred. No. 6e-0
0; Mismatches
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Query Match

86.5%;

Score 96;

ВВ 9

Length 35;

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WSHPQFEK-----XXXXXXXXXXWSHPQFEK 25 WSHPOFEKGGGSGGGSGGGSGGGSWSHPOFEK

Conservative

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Indels

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Gaps

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RESULT 3
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Best Local Similarity
Matches 16; Conserv
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                                                                            The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-x where x = Gln, Asn or Met. (I), which containing exceptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein as [PP], also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Region
                                                                                                                                                                                                                                                                                                                  New isolated peptide, useful as protein, comprises at least two modules.
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                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptavidin;
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                                                                                                                                                                                                                                                                                        Claim 8; Page 16; 18pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= GGGS_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "GGGS repeats 2-5 optionally absent,
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               86.0%;
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Score 95.5; Di
Pred. No. 3.7e:
9; Mismatches
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                affinity purification tag for recombinant high-affinity streptavidin-binding
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              ) DB 6;
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                             Length 36;
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RESULT 4
ADS20243
disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAMTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAMTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The protein of the invention demonstrates osteopathic, antinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of the human aggrecanase ADAMTS4 mutant E3620 protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; reprolysin; zinc metalloprotease; aggrecanase; osteopathic; antiinflammatory; antiarthritic; antirheuma cytostatic; osteoarthritis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease;
                                                                                                                                                                                                                          Claim 9; SEQ ID NO 40; 117pp; English.
                                                                                                                                                                                                                                                       treating aggrecanase-associated
                                                                                                                                                                                                                                                                     New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity for
                                                                                                                                                                                                                                                                                                                WPI; 2004-143860/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2002; 2002US-0398721P.
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GEORGIADIS K :
LAVALLIE E R.
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MCDÓNAGH T.
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Georgiadis KE,
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           tag
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             aggrecanase ADAMTS4 mutant E362Q protein with
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Lavallie ER;
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RESULT 5
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Matches
                    of the lipocalin family by mutation of amino acids in the region of the 4 peptide loops (at one end of the cylindrical 'leaflet' structure). Anticalins can bind to a predetermined ligand with determinable affinity. Anticalins or fusions of anticalins, are used: (a) when immobilized, for separation; and (b) when labeled, for identification of ligands (or their fusions or conjugates). Typically they bind to tissue or tumor-specific surface molecules and can be used for tumour imaging or directly for tumour therapy. Mutations can be introduced into lipocalin polypeptides more easily than into antibodies, since lipocalin polypeptides have only 4 (contrast 6) sequence segments. The peptide loops can tolerate amino acid changes without significant effect on folding. Anticalins have high specific affinity, comparable with that for antibodies. This sequence represents a fusion polypeptide used in the method of the invention
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                                                                                                                                                                                                                                      Disclosure; Page 70-72; 80pp; German.
                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                             This invention describes the preparation of anticalins from polypeptides
                                                                                                                                                                                                                                                                 New anticalins produced by mutation of lipocalin family protein
                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                          25-SEP-1998;
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/note= "This fusion peptide is constructed from
binding protein and a strep-Tag II region."
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Pred. No. 5.8;
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Query Match Best Local Similarity

61.3%;

Score Pred.

No. DB 2.2;

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Length 205

Sequence

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              This invention describes the preparation of anticalins from polypeptides of the lipocalin family by mutation of amino acids in the region of the 4 peptide loops (at one end of the cylindrical 'leaflet' structure).

Chaticalins can bind to a predetermined ligand with determinable affinity. Anticalins or fusions of anticalins, are used: (a) when immobilized, for geparation; and (b) when labeled, for identification of ligands (or their fusions or conjugates). Typically they bind to tissue- or tumor-specific surface molecules and can be used for tumour imaging or directly for tumour therapy. Mutations can be introduced into lipocalin polypeptides more easily than into antibodies, since lipocalin polypeptides have only a (contrast 6) sequence segments. The peptide loops can tolerate amino acid changes without significant effect on folding. Anticalins have high specific affinity, comparable with that for antibodies. This sequence represents a fusion polypeptide used in the method of the invention
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                                                                                                                                                                                                                                                                       New anticalins produced by mutation of lipocalin family protein
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                                                                                                                                                                                                                                            Disclosure; Page 73-74; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                              (SKER/) SKERRA A.
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/label fusion_peptide
/label "This fusion peptide is constructed from bilin
/note= "This fusion peptide is constructed from bilin
binding protein, a strep-Tag II region and the G prote
albumin binding domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
206. .:
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/note= "bilin binding protein"
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                                                                                                                                                                                                                                                                                        This invention describes novel polypeptides (I) that are muteins of bilin-binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being used as a label. Compared with Dig-specific antibodies, (I) have a simpler structure and are easier to prepare. They have very high specificity for Dig, relative to other steroids, and fusion partners may be attached to either end without compromising their ability to bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bilin-binding protein; mutein; BBP; digoxigenin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bilin binding-protein associated protein #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 59-60; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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DB; AAF25703.
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  183
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9; Conserv
  YSDFSEAACKVNNSNWSHPQFEK 205
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                                                                                                                                                                                                           of the lipocalin family by mutation of amino acids in the region of the 4 peptide loops (at one end of the cylindrical 'leafler' structure). Anticalins can bind to a predetermined ligand with determinable affinity. Anticalins or fusions of anticalins, are used: (a) when immobilized, for separation; and (b) when labeled, for identification of ligands (or their fusions or conjugates). Typically they bind to tissue or tumor-specific surface molecules and can be used for tumour imaging or directly for tumour therapy. Mutations can be introduced into lipocalin polypeptides more easily than into antibodies, since lipocalin polypeptides have only (contrast 6) sequence segments. The peptide loops can tolerate amino acid changes without significant effect on folding. Anticalins have high specific affinity, comparable with that for antibodies. This sequence represents a fusion polypeptide used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 67-69; 80pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anticalins produced by mutation of lipocalin family protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAXZ4099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW93966;
                                                                                                                                                                     Sequence 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes the preparation of anticalins from polypeptides of the lipocalin family by mutation of amino acids in the region of the 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09916873-A1
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/note= "This fusion peptide is constructed
/note= "This fusion peptide is constructed
binding protein, a strep-Tag II region and
phage coat protein pIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                     This invention describes novel polypeptides (I) that are muteins of bilin binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being used as a label. Compared with Dig-specific annibodies, (I) have a simpler structure and are easier to prepare. They have very high specificity for Dig, relative to other steroids, and fusion partners may be attached to either end without compromising their ability to bind
              06-APR-2001
                                                                                                                                                                                                                                                  Sequence 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    digoxigenin.
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                                          AAB46423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                     Bilin-binding protein; mutein; BBP; digoxigenin
                              08-JUN-2000; 2000WO-DE001873
                                                                                               14-DEC-2000
                                                                                                                                                   W0200075308-A1
                                                                                                                                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                Bilin binding-protein associated protein #6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes novel polypeptides (I) that are muteins of bilin binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being used as a label. Compared with Dig-specific antibodies, (I) have a simpler structure and are easier to prepare. They have very high be attached to either end without compromising their ability to bind lideand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB46425 standard; protein; 448
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New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for digoxigenin.
                                                                                                                WPI; 2001-071071/08
N-PSDB; AAF25711.
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-binding protein (BBP), which can bind digoxigenin (Dig) or its
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RESULT 13
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Best Local
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This invention describes novel polypeptides (I) that are muteins of bilin binding protein (BBP), which can bind digoxiganin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being
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N-PSDB;
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                                                                                                                                                                                                                  Generating a mutein of human apolipoprotein D having detectable affinity to a given non-natural ligand of apolipoprotein D by subjecting apolipoprotein D to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB87310 standard;
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DB; ADB87298.
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Pred. No.
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The present invention relates to a human apolipoprotein D (ApoD) mutein (ADB87307) having detectable affinity to a given non-natural ligand of ApoD. ApoD is a member of the lipocalin family of proteins, and is involved in serum lipid transport. Mutein ADB87307 can be used as a pharmacological drug target. The present sequence, encoded by a fragment of plasmid papoD12, is a fusion protein of ApoD, a Strep-Tag II and the

is a fusion protein ain of Protein G.

Disclosure; Page 64-65;

70pp; English.

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RESULT 15
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The present invention relates to a method for generating muteins of human neutrophil gelatinase-associated lipocalin (NGAL), rat alpha2-microglobulin-related protein (A2m) or mouse 24p3/uterocalin, by subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the coat protein pIII of a filamentous bacteriophage of the M13-family or for a fragment of the coat protein. The present sequence is the protein encoded by a fragment of plasmid pHNGAL7, used to illustrate the invention. This sequence comprises human hNGAL, a Strep-Tag II and an albumin binding domain of Protein G.
                                                                                                                                                                    Disclosure; Page 59-61; 68pp; English.
                                                                                                                                                                                                 Generating a mutein of a protein for validating the protein as drug target by subjecting the protein to mutagenesis at sequence positions corresponding to sequence positions of the human neutrophil gelatinaseassociated lipocalin.
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N-PSDB; ADA27287.
                                                                                                                                                                                                                                                                                                            Skerra A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutein, human, neutrophil gelatinase-associated lipocalin, hNGAL, rat, alpha2-microglobulin-related protein, A2m, mouse, 24p3, uterocalin.
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Tag II and albumin binding domain"
22. .199
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Perfect score:
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                                                                                                                                                                                                                                                                                    Score
99.5
95.5
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seq length: 2000000000
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1: /cgm2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

3: /cgm2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgm2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgm2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

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10: /cgm2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

12: /cgm2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

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15: /cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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10S-09-809-517A-30

10S-09-809-517A-33

16 US-10-628-432-27

10S-10-628-432-27

15 US-10-628-432-27

15 US-10-628-432-27

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                               Sequence 3, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 40, Appl
Sequence 30, Appl
Sequence 33, Appl
Sequence 47, Appl
Sequence 27, Appl
Sequence 27, Appl
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0-437-963-1	-10-471-243-2	-10-380-132-	-10-219-810-46	-10-369-493-562	-10-437-963-20015	-10-424-599-184	-10-424-599-18476	-10-437-963-10406	0-437-963-14298	-10-424-599-17137	10-424-599-27	09-884-767A-	-10-358-2	-10-354-983	-10-026-578B-4	-10-767-701-4	-10-628-432-5	-09-977-137A	-09-977-137A-1	-09-977-137A-1	-09-977-137A-	-09-977-137A-	-09-977-137A-	-09-977-137A-	-09-977-137A-	US-09-977-137A-4	-10-887-228A-	-10-887-228A-	US-10-887-228A-1
Sequence 47, Appr Sequence 196479, Sequence 63501, A	4 2	e 2:	equence 46	56	U	Sequence 1840	w	w		w	w		equence	equence 8,	equence	equence 42:	equence 53,	о о,	equence	equence 11	equence 10	equence 9,	е 8,	equence 7,	equence 5,	equence 4,	equence 5,	e 9,	Sequence 1, Ap

### ALIGNMENTS

US-10-026-578B-3

Sequence 3, Application US/10026578B Publication No. US20030083474A1

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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 24
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IBA (GmbH)
APPLICANT: Gobmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity T:
TITLE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOPTWARR: Datentin version 3.1
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                                                                                                     FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (10)..(10)
OTHER INFORMATION: X represents
                                                                                                                                                                                             FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: X represents a single amino acid at the position indicated
                                                                                                                                                                                                                                                                                           ORGANISM: Artificial sequence FEATURE:
OTHER INFORMATION: Synthetic Peptide
              PEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (11)...(11)
OTHER INFORMATION: X represents a single
FEATURE
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                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/10026578B Publication No. US20030083474A1
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                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/026,578B CURRENT FILING DATE: 2002-11-11 PRIOR APPLICATION NUMBER: DE 101 13 776.1 PRIOR FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: PCT/EP01/11846 PRIOR APPLICATION NUMBER: PCT/EP01/11846 PRIOR FILING DATE: 2001-10-12 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 EQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
                                                                                                                                                     NAME/KEY: MISC_FEATURE LOCATION: (9)..(28)
OTHER INFORMATION: X represents a single amino acid at each of the positions indicat OTHER INFORMATION: ed; some of the amino acids may be missing. Where amino acids are OTHER INFORMATION: missing, the total numbers of x will be no less than 5
                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
                                                                                                                                                                                                                                                                                         LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                    OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature OTHER INFORMATION: Artificial Sequence represents
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LOCATION: (15)..(15)
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OTHER INFORMATION: X represents a single
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OTHER INFORMATION: X represents a
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US-10-628-432-40
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US-10-026-578B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: MAIO1378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 40, Application US/10628432 Publication No. US20040142863A1 GENERAL INFORMATION:
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Matches
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LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
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CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 .776.1
PRIOR PILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 101 13 .776.1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCTOR POINT PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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OTHER INFORMATION: ADAMTS4 ASM with insertion
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LOCATION: (9)..(28)
OTHER INFORMATION: Of the five
OTHER INFORMATION: repeats may
OTHER INFORMATION: be present
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OTHER INFORMATION: Artificial Sequence represents
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WSHPQFEKAGGWGPWGPW
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No. US20030083474A1
                                                                                                                           Conservative
                                                                                                                                                     50.0%;
   537
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                                                                                                                                                  Score 71;
Pred. No.
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Pred. No. 0
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                                                                                                                           Mismatches
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RESULT 7
US-10-628-432-49
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Best Local Similarity
Warches 9; Conserve
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US-09-809-517A-33
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US-09-809-517A-30
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                                                                                                                                                                                                                                                                                                                                                  APPLICATION: No. US20020034733Alel methods for displaying (poly)peptides/prote TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT ELLING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
SOFTWARE: Patentin version 3.0
SEQ ID NO 33
LENGTH: 22
TYPE: PRT
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PARENT NO. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: NO. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
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PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
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CURRENT FILING DATE: 2001-03-15
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TYPE: PAT
ORGANISM: artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: synthetic module
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                                                                                                           EFDYKDDDDKGAPWSHPQFEK 22
    Application US/10628432
                                                                                                                                                                                                Conservative
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APPLICANT: Wyeth
ITITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 47
LENGTH: 485
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; Sequence 47, Application US/10628432
; Publication No. US20040142863A1
; GENERAL INFORMATION:
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Sequence 27, Application US/10628432

Publication No. US20040142863A1

GENERAL INFORMATION:
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Matches
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CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 858
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CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 49
LENGTH: 646
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Best Local Similarity
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TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
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ORGANISM: Artificial
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ORGANISM: Artificial
                                   ORGANISM: Artificial
                                                       TYPE: PRT
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OTHER INFORMATION: furin-processed construct
                    FEATURE:
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31.2%; Pred. No. 35;
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US-10-628-432-24
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; ORGANISM: Aspbrgillus niger N400
US-10-344-741-2
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                                                                  Matches
                                                                                                  Query Match
                                                                                                                                                                                                                                   SEQ ID NO 24
                                                                                                                                     OTHER INFORMATION: Truncated ADAMTS4 molecule -10-628-432-24
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CURRENT FILLING DATE: 2003-07-29
NUMBER OF SEO ID NOS: 53
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: No. US20040038371A1e1 Aminopeptidase FILE REFERENCE: 24615-20187.00 CURRENT APPLICATION NUMBER: US/10/344,741 CURRENT FILING: DATE: 2001-08-22 PRIOR APPLICATION NUMBER: EP/NL 00202995.7 PRIOR FILING DATE: 2000-08-23 NUMBER OF SEQ JD NOS: 27 NUMBER OF SEQ JD NOS: 27
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                                                                                                                                                                         LENGTH: 697
TYPE: PRT
ORGANISM: Artificial
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                                                                  Local Similarity
les 11; Conserv
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nes 7, conserv
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668 SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 697
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                               SHPQFEK-----XXXXXXXXXXXXXHPQFEK 25
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DSM NV
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Schuurhuizen, Paul, William
Schaap, Petrus, Johannes
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                                                                  Conservative
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                                                                                56.8%; Score 63; DB 36.7%; Pred. No. 59;
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36.7%;
                                                               11; Mismatches
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Pred. No. 38;
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                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-34
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US-09-809-517A-34
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US-09-809-517A-31
                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 25
Type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
FILE REFERENCE: MORPHO/11
                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 24
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APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 34, Application US/09809517A Patent No. US20020034733A1
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                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                             LENGTH: 25
TYPE: PRT
                                                                                                                                                                                                         ORGANISM: artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: artificial sequence
                                                                          Local Similarity 41.7%; Pred. No. 1. 105 10; Conservative
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EFEQKLISEEDLNGAPWSHPQFEK 24
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Pred. No. 1
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RESULT 14 US-10-887-228A-1

Sequence 1, Application US/10887228A Publication No. US20050037402A1

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Sequence 9, Application US/10887228A

Publication No. US20050037402A1

GENERAL INFORMATION:
APPLICANT: Schering AG

TITLE OF INVENTION: Device and Process for Direct Quantitative in vitro Detained of Invention: Substance That is Contained in a Sample
FILE REFERENCE: S30569US

CURRENT APPLICATION NUMBER: US/10/887,228A

CURRENT PILING DATE: 2004-07-09

PRIOR APPLICATION NUMBER: US /3 31 093.2

PRIOR APPLICATION NUMBER: US 60/478,262

PRIOR FILING DATE: 2003-07-16

NUMBER OF SEQ ID NOS: 12

SOFTWARE: PatentIn version 3.1

SOFTWARE: PatentIn version 3.1
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CURRENT APPLICATION NUMBER: US/10/887,228A
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: DE 103 31 093.2
PRIOR FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 60/478,262
PRIOR FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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Search completed: March Job time : 80.7439 secs
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US-10-887-228A-9
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                                                                                                                                                                                             Query Match 56.3%; Score 62.5; DB 17; Length 246; Best Local Similarity 41.7%; Pred. No. 20; Matches 10; Conservative 11; Mismatches 0; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 56.3%; Score 62.5; DB 17; Length 245; Best Local Similarity 41.7%; Pred. No. 20; Matches 10; Conservative 11; Mismatches 0; Indels 3
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TYPE: PRT
ORGANISM: artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schering AG
TITLE OF INVENTION: Device and Process for Direct Quantitative in vitro Determination TITLE OF INVENTION: Substance That is Contained in a Sample
                                                                                                                                                                                                                                                                                                                                                    ORGANISM: artificial FEATURE:
                                                                                             223 EFECKLISEEDLNGAPWSHPQFEK 246
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Maximum Match 100%
Listing first 45 summaries
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            Sequence 30, Appl Sequence 31, Appl Sequence 31, Appl Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence
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Sequence 8	Sequence 8	Sequence 4,	Sequence 3	Sequence 5	Sequence 5	Sequence 5	Sequence 9,	Sequence 5,	Sequence 9	Sequence 8,	Sequence 7,	Sequence 2	Sequence 2	Sequence 2	Sequence 5	Sequence 3	Sequence 9
817, App	874, App	, Appli	<ol> <li>Appli</li> </ol>	55, Appl	55, Appl	55, Appl	, Appli	, Appli	, Appli		-	, Appli	26479, P	26513, A	50987, A	35770, A	995, App

US-09-809-517A-30

### GENERAL INFORMATION: APPLICANT: Lohning, Corinna TITLE OF INVENTION: No. 6753136el methods for displaying (poly) peptides/proteins on b TITLE OF INVENTION: particles via disulfide bonds FILE REFERENCE: MORPHO/11 CURRENT APPLICATION NUMBER: US/09/809,517A CURRENT FILING DATE: 2001-03-15 PRIOR APPLICATION NUMBER: EP 09114072.4 PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR FILING DATE: 2000-02-18 NUMBER OF SEQ ID NOS: 41 SEQ ID NO 30 LENGTH: 21 TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: PRI TYPE: 밁 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-30 RESULT 2 US-09-809-517A-33 S Sequence 30, Application US/09809517A Patent No. 6753136 Matches Query Match ORGANISM: artificial sequence FEATURE: Match 61.3%; Score 68; Local Similarity 42.9%; Pred. No. 9; EFDYKDDDDKGAPWSHPQFEK 21 Conservative 11; Mismatches 0 DB 4; .009; 1; Indels Length 21; <u>.</u> Gaps 0 9

Sequence 33, Application US/09809517A
Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
FILE REFERENCE: MORPHO/11

CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 0103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41

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RESULT 4
US-09-809-517A-34
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                         NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENGTH: 25
TYPE: DOT
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Patent No. 6753136
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Best Local
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Patent No. 6753
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                                                                                                                    APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly).peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
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CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
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NUMBER OF SEQ ID NOS: 41
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ORGANISM: artificial sequence
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-809-517A-34
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                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTMARE: PATENTIN Ver. 2.0
SEQ ID NO 5
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Patent No. 6750042
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Best Local Similarity
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                    FILE REFERENCE: 79-00
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TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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                                                                                       OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
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TYPE: PRT
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             Score 62; DB 4; Pred. No. 0.75; 0; Mismatches
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Pred. No. 0.75;
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Pred. No. 0.
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US-09-977-137A-7
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                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09977137A
PALENT NO. 6750042
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 799-00
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SEQ ID NO 7
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 117
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                                                                                             Query Match
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
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                                                                                                                                                                                                 TYPE: PRT
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les 8; Conserv
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                                                                 Conservative
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                                                                             Score 62;
Pred. No.
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RESULT 9

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RESULT 11
US-09-977-137A-11
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US-09-977-137A-10
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TITLE OF INVENTION: Methal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT PILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 117
TYPE: PRT
Sequence 11, Application US/09977137A
Patent No. 6750042
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
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Best Local !
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SEQ ID NO 9
LENGTH: 117
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Best Local Similarity
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APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonath
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CURRENT APPLICATION UMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
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les 8; Conservative
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                                                                                                                                                                                                                                                                              55.9%; Score 62; I
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APPLICANT: Summers, Anne O.
APPLICANT: Cagulat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Re
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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US-09-977-137A-12
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                                                                                                                                                                                                         Sequence 6, Application US/09977137A Patent No. 6750042
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
TENETTH: 117
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Best Local
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SEQ ID NO 12
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Best Local Similarity
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ 1D NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Caggulat, Jonathan
TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
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APPLICANT: Caquiat, Jonath
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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NUMBER OF SEQ ID NOS:
; SOFTWARE: Patentin Ve:
; SEQ ID NO 2
; LENGTH: 318
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US-08-828-741B-11
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                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08828741B Patent No. 6043069
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GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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SEQ ID NO 6
LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DellaPenna, Dean
APPLICANT: Shintani, David
TITLE OF INVENTION: Wanipulation of Tocopherol
FILE REFERENCE: 920905.90032
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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TYPE: PRT
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OTHER INFORMATION: Description of Artificial Sequence:
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          ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                TITLE OF INVENTION: CATALYTIC ANTIBODIES AND TITLE OF INVENTION: PRODUCING SAME
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                    APPLICANT: Koentgo
APPLICANT: Suess,
                                                                                                                                               ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 38.9%; Score 55; DB es 7; Conservative 10. ...
                                                                                                                COUNTRY:
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                                                                                                                                 New York
                                                                                                                United States of America
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Treutlein, Herbert
VENTION: CATALYTIC
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44.4%; Pred. No. 0.
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               Version #1.30
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Page 5

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APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE,DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-43436
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 155 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: 1inear
MOLECULE TYPE: protein
US-08-828-741B-11

48.6%: Score
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Search completed: March 2, 2005, 12:25:37 Job time: 28.4553 secs
                                                                                                                                                                              Query Match 48.6%; Score 54; DB 3; Length 155; Best Local Similarity 34.8%; Pred. No. 16; Matches 8; ¡Conservative 10; Mismatches 5; Indels
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131 YSPGQGTKLEIKRSGSAWRHPQF 153
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Maximum Match 100%
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Maximum DB
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2005 Compugen Ltd
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125.901 Million cell updates/sec
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C;Species: Homo sapiens (man)
C;Date: 02-Jun-1995 #sequence_revision 02-Jun-1995 #text_change 09-Jul-2004
C;Accession: A54660
R;Hofmann, S.L.; Topham, M.; Hsieh, C.L.; Francke, U.
Genomics 9, 656-669, 1991
A;Title: CDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein,
A;Reference number: A54660; MUID:91244309; PMID:2037293
A;Accession: A54660.
A;Experimental source: BAC clone B23II1; strain OR74A C;Genetics:
A;Gene: NCSP:B23II1.60
A;Map position: 6
A;Introns: 34/3; 60/3; 87/1
C;Superfamily: conserved probable membrane protein YIL003w
                                                                                         A;Status: Free: DNA
A;Molecule type: DNA
A;Mesidues: 1-331 <SCH>
A;Cross-references: EMBL;AL391572; GSPDB;GN00116; NCSP:B23I11.60
A;Cross-reference: BAC clone B23I11; strain OR74A
                                                                                                                                                                                                                                                                                                                               related to nucleotide-binding protein [imported] - Neurospora crassa N;Alternate names: protein B23I11.60 C;Species: Neurospora crassa C;Species: Neurospora crassa C;Date: 20-Oct-2000 #sequence revision 20-Oct-2000 #text_change 03-Nov-2000 C;Accession: T51894
                                                                                                                                                                                                             A;Reference number: Z25858
A;Accession: T51894
A;Status: preliminary
                                                                                                                                                                                                                                                                                      R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; submitted to the Protein Sequence Database, August
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A;Map position: 19q13.3-19q13.3
C;Keywords: calcium binding
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A;Molecule type: mRNA
A;Residues 1-699 - KHOP>
A;Cross-references: UNIPROT:P23327; GB:M60052; NID:g183918; PIDN:AAA88071.1; PID:g183912
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9; Conservative
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37.5%;
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RESULT 5
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hyporthetical protein ECs2201 [imported]
C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown protein encoded within prophage CP-9330 [imported] - Escherichia coli C;Species: Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: C85713 C;Accession: C85713 Fibrana, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D. iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K. Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q8X549; GB:AE005174; NID:g12515046; PIDN:AAG56167.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-103 < STO>
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(;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87532
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession. A87532
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A; Residues: 1-771 <STO>
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            ;Date: 18-Jul-2001
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      #sequence_revision 18-Jul-2001
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A; Gene: FAS1
C; Superfamily
C; Keywords: a
                                                      A;Cross-references: UNIPROT:P34731; EMBL:X74952; NID:g402176; PIDN:CAA52907.1; PID:g4021
C;Genetics:
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A; Residues: 1-2037 < ZHA>
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                  Superfamily:
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C;Accession: S37178
R;Zhao, X.J.; Cihlar, R.L.
submitted to the EMBL Data Library,
A;Description: Isolation and sequent
A;Reference number: S37178
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A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AI2017
                                                                                                          fatty-acyl-CoA synthase (EC 2.3.1.86) beta chain - yeast (Candida albicans) N;Alternate names: fatty-acid synthase beta chain C;Species: Candida albicans C;Species: Candida albicans C;Datc: 10-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-1449 <KUR>
A;Cross-references: UNIPROT:Q8YMCO; GB:BA000019; PIDN:BAB78061.1; PID:g17135515;
A;Experimental source: strain PCC 7120
C;Genetics:
A; Accession: S37178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein all1695 [imported] - Nostoc sp. (strain PCC (Species: Nostoc sp. PCC 7120 A;Note: Nostoc sp. errain PCC 7120 is a symonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change C;Accession: AIZ017 T.; Nakamura, Y.; Walk, C.P.; Kuritz, T.; Sasamoto, S. Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.
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A; Residues: 1-103 <HAY>
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R;Hayashi, T.; Makino,
gasawara, N.; Yasunaga,
DNA Res. 8, 11-22, 2001
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                                                                                                                                                                                                                                                                             OFEKXXXXXXXXXXXXHPQFEK 26
                                                                                                                                                                                                                                                                                                                                                            Conservative
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T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                             50.0%;
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                                   sequence
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                                                                                                                                                                                                                                                                                                                                                        Score 56; DB 2;
Pred. No. 1.3e+02;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56;
Pred. No.
                                                      September 1993
                                                                                                                                                                                                                                                                                                                   21
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RIMD 0509952
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                                   Candida
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                               albicans FAS1 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain PCC 7120
09-Jul-2004
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Tabata, S
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acyltransferase;

yeast

fatty-acyl-CoA synthase

beta

coenzyme

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A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pyruvate dehydrogenase XF0669 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
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C; Superfamily: auxin-induced protein 10A
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A;Residues: 1-98 <STO>
A;Cross-references: UNIPROT:Q9SKP2; GB:AE002093; NID:g4803922; PIDN:AAD29795.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUID:20083487; PMID:10617197 A,Accession: E84598
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R;anonymous, The Xylella fastidiosa Consortium of the Organization Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lin, X., Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Niermañ, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable auxin-regulated protein [imported] - Arabidopsis thaliana
(;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84598
A, Reference number: A59328
                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-985 <SIM>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPSFDKIYTQGLNILSWLKHPE 210
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; 18n11, K.; 10KOyama, N., 10
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA, Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99829; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Wu,
                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-103 <HAY>
A;Cross-references: UNIPROT:Q8X4V0; GB:BA000007;
A;Experimental source: strain O157:H7, substrain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F20D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #te:C;Accession: T16114
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                                                                                                                                              A;Gene:
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A;Introns: 159/1; 212/2; 263/3; 334/2; 385/1; 513/3; 754/2; 787/3;
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A; Cross-references: UNIPROT: Q19645;
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A; Residues: 1-1030 <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid
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C; Superfamily:
                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: E90973
                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ECs2757 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E90973
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Best Local S
Matches 7
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Best Local S
Matches 5
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Gene: ECs2757
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                                                                     Similarity 5; Conserv
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KEMPVERNEYGCWTHPEYEK 24
                                PQFEKXXXXXXXXXXXWSHPQF 24
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                                                                   48.2%;
llarity 25.0%;
Conservative 1
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ilarity 29.6%;
Conservative 12
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                                                                       15;
                                                                                    Score 54;
Pred. No.
                                                                     red. No. 12;
Mismatches
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                                                                                                                                                                                PIDN:BAB36180.1;
RIMD 0509952
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unknown protein encoded within prophage CP-933U [imported] C;Species: Escherichia coli

Escherichia

coli

(strain

A85821 RESULT 12

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R;Bustard, K.; Gupta, R.S.
J. Mol. Evol. 45, 193-205, 1997
A;Title: The sequences of heat shock protein 40
A;Reference number: Z22880; MUID:97383250; PMID:
A;Accession: T44957
                                                                                                                                                                                                                                                                                                                                                   RESULT 14
T44957
                   A;Residues: 1-389 <BUS>
A;Cross-references: UNIPROT:O34135; EMBL:U93357; PIDN:AAB96891.1
A;Experimental source: ATCC 33170
                                                                                                                                                                                                                                                                  C;Species: Halobacterium salinarum A;Variety: ATCC 33170
                                                                                                                                                                                                                                                                                                    heat shock protein dnaJ [similarity] - Halobacterium salinarum
N;Alternate names: 40K chaperone; 40K heat shock protein
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C; Superfamily:
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T26842
      A;Note:
                                                                            A; Molecule type: DNA
                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-363 <WIL>
A;Residues: 1-363 <WIL>
A;Cross-references: UNIPROT:045933; EMBL:AL021481; PIDN:CAA16333.1; CESP:Y43F4B.4
A;Experimental source: clone Y43F4B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP: Y43F4B.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-103 <STO>
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;Accession: T44957
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Best Local S
Matches 6
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is designated
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cutirubrum
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EDL933
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K.; Apodaca,
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Search completed: March Job time : 20.8699 secs

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12:29:00

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OVERGOLGIFNKGYWNHPEYK 177

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C;Genetics:
A;Gene: dnaJ
C;Superfamily: l
F;4-68/Domain: c
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A)Cross-references: UNIPROT:067092; GB:AE000715; NID:g2983460; PIDN:AAC07046.1; PID:g298
A:Experimental source: strain VF5
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A70383
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: A70383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70383
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                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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137.824 Million cell updates/sec
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1: uniprot_sprot:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
SUMMARIES
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Q9BBGO Q9BBG3 Q96XI8 HTPG_NITEU Q8YWCO Q7QHY8 FAS1_CANAL Q9SKP2 Q8WZX8 Q949H3	Q8P4T1 Q6Z315 Q742U3 Q742U3 Q6EQ71 Q7SAB0 Q9BLU4 Q8X549 Q8X549 Q7V8E9 Q7V8E9 Q7V8E9 Q7V8E9 Q7VNS9 MATK_MARSC	SRCH HUMAN Q7YS21 Q8CJD2 Q8CJD2 Q8CH90 Q9CH91 Q72N84 Q72N84 Q72N87 Q756P7 Q8TTK4 Q9A613	ID
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OBGUD77 OBCZN5 Q70912 Q70912 Q8EEC3 Q9PF18 Q19645 MLL3_MOUSE MLL3_HUMAN Q62ES0 Q63119 Q83119 Q83731 Q8374V0 Q63773	NYMD
	08guar 08zzn5 07g91z 09eec3 09pfia 019645 08brh4 08nez4 063119 08nt31 081219 084219

## ALIGNMENTS

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EMBL: M60052; AAA880 PIR; A54660; A54660 Genew; HGNC:5178; HRC MIM; 142705; GO; GO:0005509; F:cal GO; GO:0005509; F:cal GO; GO:0006936; P:mus Calcium-binding; Poly SIGNAL 29 69 DOMAIN 193 20 DOMAIN 193 20 DOMAIN 106 36 REPEAT 180 21 REPEAT 295 31 REPEAT 295 31 REPEAT 343 36 DOMAIN 106 34	chromosome 7."; Genomics 9:556I- FUNCTION: M sequestrati -!- SUBCELLULARITY:	Name=HRC; Synony Name=HRC; Synony Homo sapiens (Hu Eukaryota; Metaz Mammalia; Euther NCBI TaxID=966; SEQUENCE FROM N. TISSUE=Skeletal MEDLINE=91244309 Hofmann S.L., To "CDNA and genomi protein, and loco	RESULT 1 SRCH_HUMAN ID SRCH_HUMAN ID OT 01-NOV-1991 DT 01-NOV-1991 DT 01-UT-2004 DE Sarcoplasmic
3, 3, 4, 4, 6, 8, 9, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	Chromosome 7.";  Genomics 9:656-669(1991).	precursor.  Name-HRC; Synonyms=HCP;  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Crania  Mammalia; Eutheria; Primates; Catarr  NCBI TAXID=9606;  SEQUENCE FROM N.A., AND VARIANTS.  TISSUE=Skeletal muscle;  MEDLINE=91244309; PubMed=2037293;  Hofmann S.L., Topham M., Hsteh CL.  "CDNA and genomic cloning of HRC, a  grotein, and localization of the ger	STANDAR (Rel. 20, (Rel. 20, (Rel. 44, c reticulum
### ABBOV.1.1;  ### ABBOV.1.1;  ### F:calcium ion binding; TAS.  ### P:muscle contraction; TAS.  ### P:muscle contraction; TAS.  ### P:muscle contraction; TAS.  ### P:muscle contraction; TAS.  ### Barcoplasmic reticulum histidine-rich  ### Calcium-binding protein.  ### 204	sregulation of calcium SR of skeletal and cardiac mulic reticulum lumen. (C	lata; Craniata; Vertebrata; Euteleostomi; lata; Catarrhini; Hominidae; Homo:  //ARIANTS.  2037293;  Hsieh CL., Francke U.; sof the gene to human chromosome 19 and mouse	D; PRT; 699 AA. Created) Last sequence update) Last annotation update) histidine-rich calcium-binding protein

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RESULT QBCJD2
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Hong S., Cho C.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX305856; AAP70486.1;
InterPro; IRR001450; 4Fe4S_ferredoxin.
InterPro; IPR002134; HCP.
PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00128; HCP; UNKNOWN_1.
PROSITE; PS00328; HCP; UNKNOWN_1.
SPROUENCE 722 AA; 82753 MW; 87CBE737FA647F24 CRC64;
                                                                                 Guanylyl cyclase alpha 1 subunit.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eummalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID=10116;
    SEQUENCE FROM N.A. Nakamura I., Suzuk Submitted (NOV-200
                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                            Q8CJD2;
01-MAR-2003
                                                                                                                                                                                                                                                                                       Q8CJD2
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Histidine-rich calcium binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macaca fascitularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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NCBI_TaxID=9541;
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TISSUE=Heart;
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9; Conserv
    I., Suzuki N.;
1 (NOV-2002) to
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Pred. No.
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9922EEDF012C61DD CRC64;
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5 -> A (in dbsNP:3745297).
/FIId=VAR_005623.
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; Murinae; Rattus.
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
Type II DNA topoisomerase (
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SEQUENCE
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SEQUENCE
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InterPro; IPRO09080; tRNAsym 1a bind.
Pfam; PF00211; Guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
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GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Soluble guanylyl cyclase alpha 2 subunit E219G mutant.
Rattus norvegicus (Rat).
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PROSITE;
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HSSP; P30803; IAZS.
GO; GO:0004383; F:guanylate cyclase activity; IEA.
GO; GO:00016829; F:lyase activity; IEA.
GO; GO:0007242; P:intracellular signaling cascade;
InterPro; IPR001054; G_cyclase.
Pfam; PF00211; Guanylate cyc; 1.
ENGRET; SM00044; CYC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00452; GUANYLATE CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura I., Yao Y., Suzuki N.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB097860; BAC44887.1; -...
HSSP, P30803; 1AZS.
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01-MAR-2003
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8; Conserv
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   743 AA;
                                                                                    (TremBirel. 16, Created)
(TremBirel. 16, Last sequence update)
(TremBirel. 25, Last annotation updat
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                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.5%;
llarity 44.4%;
Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83251 MW; ACF5C53E0982813A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 61;
Pred. No.
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Pred. No.
                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F73FC97B68544E6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 743;
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Name=top2;

Eukaryota; Fungi; Ascomycota;

(Candida guilliermondii).
Saccharomycotina; Saccharomycetes;

Pichia guilliermondii (Yeast)

(Fragment).

update)

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RESULT
Q72NB4
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relax only negative supercoils (By Similarity).

- :- SIMILARITY: Belongs to the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoisomerase for the type II topoiso
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Q72N84;
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                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Dipeptide/oligopeptide ABC transport system permease protein.
OrderedLocusNames-LIC12953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales; Saccharomycetaceae; Pichia.
NCBI_TaxID=4929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ÷
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STRAIN=Fiocruz L1-130;
PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           +
                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; DNA-binding; Isomerase;
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=44275
                                                                                                                                                                                                                                                    Copenhageni
                                                                                                                                                                                                                                                                                     eptospira interrogans (serogroup Icterohaemorrhagiae / serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          breakage and subsequent rejoining of DNA strands.
makes double-strand breaks (By similarity).
CATALYTIC ACTIVITY: ATP-dependent breakage, passac of double-stranded DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax bo negative and positive supercoils, whereas prokaryotic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Control of topological states of DNA by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of double-stranded DNA.
SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wshpqfekxxxxxxxxxxxxshpqfe
                                                                                                                                                                                                                    Spirochaetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      782
782
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                                                                                                                                                                                                                Spirochaetales; Leptospiraceae; Leptospira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OB9CFDB3BDAABA6D CRC64;
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RESULT 7
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RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutlinbo L.L., Degrave W.M., Dellagostlin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Giglioti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo I.L.M., Kimura E.T.,
RA Goliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.B.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
"Comparative genomics of two Leptospira interrogans serovars reveals
"Comparative genomics of two Leptospira interrogans serovars reveals
"Comparative Jenomics of two Leptospira interrogans serovars reveals
"Comparative Jenomics of two Leptospira interrogans serovars reveals
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"Comparative Jenomics of
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Matches 7
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Q8F8C3;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
MEDLINE=22598143; PubMed=12712204; DOI=10.1036/nature01597;
Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
Jiang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
Zhang Y., Zhu G.-F., Wann M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Yao Z.-J., Shen Y., Qiang B.-Q., Xia Q.-C., Guo X.-K., Danchin A.,
Yao J.-G., Zhao G.-P.,
Xu J.-G., Zhao G.-P.,
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01-MAR-2003 (TYEMBLrel. 25, Last sequence update)
01-MAR-2004 (TYEMBLrel. 26, Last annotation update)
Dipeptide/oligopeptide/nickel transport systems, pe
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-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity)-
-!- SIMILARITY: Belongs to the binding-protein-dependent transport system permease family.
EMBL, AE017298; AAS71503.1; --
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:0006810; P:transport; IEA.
InterPro; IPR000515; BPD transp.
system permease family.
EMBL; AE011250; AAN47833.1;
GO; GO:0016021; C:integral
                                                                                                                                  -:- FUNCTION: Part of a binding-protein-dependent tran 
Probably responsible for the translocation of the 
the membrane (By similarity) 
-:- SUBCELLULAR LOCATION: Integral membrane protein (E 
-:- SIMILARITY: Belongs to the binding-protein-depende
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Bacteria, Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
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253 AA;
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PSS0928; ABC_TM1; 1.
proteome; Transmembrane; Transport.
253 AA; 27677 MW; 0A145ACBE801964C_CRC64;
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         membrane; IEA
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-i- CAUTION: The sequence shown here EMBL/GenBank/DDBJ whole genome sh
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PROSITE; PS50928; ABC_TM1; 1.

Complete proteome; Transmembrane; Transport.

SEQUENCE 253 AA; 27677 MW; 0A145ACBE801964C CRC64;
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Name=NCU04788.1;
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7; Conserv
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RA Galagan J.S., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh M., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A., Guss A.M.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic RL Edenome Res 1.2:53.2-42(2002).
DR EMBL, ABOl0703, AAM03874.1; -.
DR GO: GO: non-2-2-
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Q9A613
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01-JUN-2001
01-OCT-2003
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PRODOM; PD000288; Aldo/Ket red; 1.

PROSITE; PS00198; 4FE4S_PERREDOXIN; 1.

4Fe-4S; Complete proteome; Iron; Iron-sulfur; Metal-binding.

SEQUENCE 400 AA; 45143 MW; 7FAD17732FE7DC29 CRC64;
                                                                                                                                                                                                                                               OrderedLocusNames=CC2282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005489; F:electron transporter activity; GO; GO:0005506; F:iron ion binding; IEA. GO; GO:0006118; P:electron transport; IEA. Pfam; PF000348; Aldo ket red; 1. Pfam; PF00037; Fer4; 1.
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Methanosarcina acetivorans.
Archaea; Buryarchaeota; Methanomicrobia; Methanosarcinales;
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Pred. No.
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MEDLINE-21173698; PubMed-11259647; DOI=10.1073/pnas.061029298; Misrman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J., Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Vamathevan J.J., Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J., Berry G.M., White O., Salzberg S.L., Venter J.C., Shapiro L.,

ø

"Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). EWBL; AE005898; AAK24253.1; -.

Fraser C.M.;

SEQUENCE FROM N.A. STRAIN=ATCC 19089 / CB15;

Bacteria; Proteobacteria; Alph Caulobacteraceae; Caulobacter.

Alphaproteobacteria; Caulobacterales;

Caulobacter crescentus.

NCBI\_TaxID=155892;

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RESULT 11
Q8P4T1
ID Q8P47
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RP SEQUENCE FROM N.A.

RC STRAIN-ATCC 33913 / NCPPB 528;

RX MEDLINE-22022145; Pubmede-12024217; DOI=10.1038/417459a;

RX MEDLINE-22022145; Pubmede-12024217; DOI=10.1038/417459a;

RX MEDLINE-22022145; Pubmede-12024217; DOI=10.1038/417459a;

RX MEDLINE-22022145; Pubmede-12024217; DOI=10.1038/417459a;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

RA Camarottte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martine E.C., Machado M.A., Maddira A.M.B.N., Martinez-Rossi N.M.,

RA Martine E.C., Machado M.A., Maddira A.M.B.N., Martinez-Rossi N.M.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Findade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Schubal J.C., Kitajima J.P.,

RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";

RT "Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.";

RM BELL RAMAYASSI.; -.

RM INTERPROSA J. ANAMASSSI.; -.

RM INTERPROSA J. ANAMASSSI.; -.

RM INTERPROSA J. Transketolase N.;

RM INTERPROSA J. Transketolase N.;

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SEQUENCE
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01-OCT-2002 (TrEMBLrel. 22, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last annot
Pyruvate dehydrogenase.
Name=aceE; OrderedLocusNames=XCC3625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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SEQUENCE 771 AA; 82468 MW; D554EC477C4E4409
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InterPro; IPR006425; Glucan_glucosid.
InterPro; IPR008928; Glyco_trans_6hp.
TIGRFAMs; TIGR01535; glucan_glucosid; 1.
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HSSP; O85672; 1LF6.
TIGR; CC2282; -.
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WSCPSFNELRRDGFDAERWNRLHPEAEQ 791
                                    WSHPQFEKXXXXXXXXXXWS--HPQFEK 26
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                                                                      Score 58; DB
Pred. No. 3e+0
14; Mismatches
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Pred. No. 1.9e
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3e+02;
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Q742U3;
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
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Q6Z315;
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
DCL protein-like.
                                                                                                                                                                                                                                                                                                                                                    Li L., Bannantine J., Zhang Q., Amonsin A., Alt D., Kapur V.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AE017229; AAS03059.1; -
GO; GO:0001760; F:aminocarboxymuconate-semialdehyde decarboxy.

GO; GO:0008152; P:metabolism; IEA.
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Oryza sativa (japonica cultivar-group)
Cukza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Spermatroideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T. Matsumoto T., Yamamoto K.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
EMBL; AP005287; BAD17315.1; -.
EMBL; AP004817; BAD17127.1; -.
                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 380 AA;
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OrderedLocusNames=MAP0742c;
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Submitted (MAY-2002)
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NCBI_TaxID=1770;
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9; Conservation
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WAGHPYMAQILIKAEPRPSWGHPKYD
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                                                                                                                                            51.3%;
llarity 23.1%;
Conservative 15
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the EMBL/GenBank/DDBJ
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RESULT 14 Q6EQ71 ID Q6EQ7 AC Q6EQ7

Q6EQ71;

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RESULT 15
Q7SAB0
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Matches 6
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Matches 7
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein OSJNBa0017118.11 (Hypothetical
OSJNBb0095104.17)
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Q75AB0;
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AP005724; BAD29199.1; -.
EMBL; AP005701; BAD29131.1; -.
Hypothetical protein.
SEQUENCE 202 AA; 22026 MW; 23392FDF138284FB CRC64;
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Oryza sativa (Japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                         preliminary data.
EMBL; AABX01000205; EAA33347.1;
SEQUENCE 1111 AA; 121374 MW;
                                                                                                                                                                                                                                                                                                   Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Eukaryota, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
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STRAIN=OR74A;
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Name=NCU06321.1;
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Search completed: March 2, 2005, 12:44:29 Job time : 97.6016 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

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protein, modules.

Disclosure; Page 4; 18pp; German.

WPI; 2003-031166/03.

New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding

The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. ), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily

<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26
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Ado25157 Melanoma	Ads17525 Amino aci	Adr28054 NPB polyp	Adr70386 Polioviru	Adr70319 Polioviru	Adr70385 Polioviru	Adr70320 Polioviru	Aau01630 Human sec	Adl77623 Albumin f	Adl77621 Albumin f	Adf10783 Human sec	Adc20522 Human sec	Ada44167 Human sec	Ada98358 Human sec	Abg64356 Human alb	Abg64354 Human alb	Aae04132 Human gen	Aae04104 Human gen	Adp18461 Arthrobac	Ada00703 Modified

## ALIGNMENTS

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RESULT 2
ABP60369
ID ABP6
               The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain Streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proceins (FP), also for detecting FP, Ce.g. on protein chips or microtitre plates. The modules in (I) bind Strongly to streptavidin, with a co-operative effect that provides strongly to streptavidin, with a co-operative effect that provides Stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
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Matches 24
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                                                                                                                                                                                                                                                                        Claim 7; Page 16; 18pp; German
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Pred. No. 9.7e-06;
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ABP60370
ID ABP6
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Matches 26; Conserv
                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                                                                                                                                                                                                                           Claim 8; Page 16; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                    New isolated peptide, useful as protein, comprises at least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-2001; 2001DE-01013776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2001; 2001DE-01013776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptavidin
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-031166/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE10113776-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABP60370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP60370 standard; peptide;
                                  16;
                                              Similarity
WSHPQFEK-----XXXXXXXXXXXXWSHPQFEK 26
                                                                                        36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WSHPQFEK-----XXXXXXXXXXXXXWSHPQFEK 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding peptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein chip; microtitre plate; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= GGGS_repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                           86.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "GGGS repeats
                                             Score
Pred.
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                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                 affinity purification tag for recombinant high-affinity streptavidin-binding
                                             97;
No.
                          DB 6; bu.
3.2e-05;
0;
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                                                        Length
                                Indels
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                                                          36;
                              10;
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                             Gaps
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ADD19011 ADD19011 ADD19011 ADD19011 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901 ADD1901
RESULT 5
ADO19053
ID ADO1
XX
AC ADO1
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a non-competitive immunoassay for a small canalyte, comprising reacting a sample containing the analyte with a reagent pair comprising a first binding partner that binds to the analyte and a second binding partner that binds to the complex of the analyte and the first binding partner, and determining the binding of the second binding partner, and determining the binding of the second binding partner, thus indicating the presence of the analyte in the sample. The first and second binding partners are antibody fragments Fab or scFv. The reagent pair is useful in a non-competitive immunoassay for a small analyte, particularly for assaying drugs of abuse e.g., morphine, THC or amphetamine. The immunoassay is useful for detecting environmental hazards, toxic compounds in food and feed, chemicals indicative of congoing processes (e.g., microbial processes in buildings, metabolic processes of living organisms) and in clinical tests, drug monitoring and pharmacological research. This sequence represents the murine antibody MI Fab fragment heavy chain, used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; antibody; M1 Fab; heavy chain; Fab; scFv; abused drug; morphine; THC; amphetamine; environmental hazard; toxic compound; microbial process; metabolic process; drug monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AD019051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADO19051 standard; protein; 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; SEQ ID NO 2; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-competitive immunoassay for small analyte, useful for assaying dof abuse (e.g., morphine), comprises reacting a sample of analyte wireagent pair comprising a first binding partner and a second binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-420710/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-2002; 2002FI-00002048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  de snw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-AUG-2004 (first entry)
                               ADO19053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-NOV-2003; 2003WO-FI000875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004046733-A1
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                                                                                                  ADO19053 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VALW ) VALTION TEKNILLINEN TUTKIMUSKESKUS.
                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                        AHPASSTKVDKKIVPRDCGTSWSHPQFEK 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoeyhtyae M, Takkinen K,
                                                                                               protein; 236
                                                                                                                                                                                                                                                                                                                                                                                                                                   64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB (
Pred. No. 1.1;
13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 236
                                                                                                                                                                                                                                                                                                                                                                                                       4; .Gaps
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RESULT 6
ABP60363
ID ABP6
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XX Synt
                                                                                                                                                                                                                                                                                                                                                                                                    cc analyte, comprising reacting a sample containing the analyte with a cc reagent pair comprising a first binding partner that binds to the analyte and the first binding partner that binds to the analyte and the first binding partner, and determining the binding of the second thinding partner, and determining the binding of the second cc binding partner, thus indicating the presence of the analyte and the complet. The first and second binding partners are antibody fragments Fab cr sefv. The reagent pair is useful in a non-competitive immunoassay for a small analyte, particularly for assaying drugs of abuse e.g., morphine, cc manufacture of the analyte and the compounds in food and feed, chemicals indicative of compoing processes (e.g., microbial processes in buildings, metabolic compounds in food and in clinical tests, drug monitoring and comparancological research. This sequence represents the murine antibody M2 Fab fragment heavy chain, used in the method of the invention.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; antibody; M2 Fab; heavy chain; Fab; scFv; abused THC; amphetamine; environmental hazard; toxic compound; microbial process; metabolic process; drug monitoring;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 21; SEQ ID NO 4; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-competitive immunoassay for small analyte, useful for assaying drug of abuse (e.g., morphine), comprises reacting a sample of analyte with reagent pair comprising a first binding partner and a second binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-420710/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pulli T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-2002; 2002FI-00002048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JUN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pharmacological research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine antibody M2 Fab fragment heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-AUG-2004 (first entry)
                Synthetic
                                                Streptavidin;
                                                                                Streptavidin
                                                                                                                                              ABP60363;
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                                                                                                                28-MAR-2003
                                                                                                                                                                            ABP60363 standard;
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                                                                                                                                                                                                                                                            208 AHPASSTKVDKKIVPRDCGTSWSHPQFEK 236
                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                          Hoeyhtyae M,
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                              binding peptide SEQ ID
                                                                                                              (first
                                                protein chip; microtitre plate;
                                                                                                                                                                            peptide;
                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                         64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takkinen K,
                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                             24
                                                                                                                                                                                                                                                                                                                                         Score 72; DB
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                        8
                                                   detection
                                                                                                                                                                                                                                                                                                                          1:
                                                                                                                                                                                                                                                                                                                                                      Length 236;
                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 7
ADA00709
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Best Local S
Matches 21
              Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Prox where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein set (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                                                                        Synthetic.
                                                                                            mutein; human neutrophil gelatinase-associated lipocalin; hNGAL; rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin; 24p3; mutagenes1s; fusion protein; cytostatic; gene therapy; tumour imaging; cancer therapy.
                                                                                                                                                                     Modified hNGAL related fusion protein
                                                        Homo sapiens
                                                                                                                                                                                                  06-NOV-2003 (first entry)
                                                                                                                                                                                                                                                         ADA00709 standard; protein; 209
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated peptide, protein, comprises at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-031166/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001DE-01013776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DE10113776-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                              1 WSHPQFEKXXXXXXXXXXXXXXXSHPQ 23
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                              WSHPQFEKXXXXXXXXXXX--HPQ 21
                                                                                                                                                                                                                                                                                                                                                                                                                                              A.
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 4; 18pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIOANALYTIK GMBH GOETTINGEN.
Location/Qualifiers
1. .21
/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
9..18
/label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22. .24
/label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful as
least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      German
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Pred. No. 0.08
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      affinity purification tag for recombinant high-affinity streptavidin-binding
                                                                                                                                                                      SEQ ID NO:22
                                                                                                                                                                                                                                                                                                                                                                                                 DB 6;
0.084;
                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                              Length 24;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT 8 ADA27293 ID ADA2

ADA27293 standard; protein; 258

B

밁 S

185

NHIVFPVPIDQCIDGSAWSHPQFEK 209

26

Matches Query Match Best Local

l Similarity 10; Conserv

Conservative

60.7%; pre/ 40.0%; pre/

Score 68; DB pred. No. 3.4; L1; Mismatches

6

Length 209

0;

Gaps

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C given target, comprising subjecting the protein to mutagenesis at the positions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in mutagenesis at the protein. Also described: (1) a mutagenesis at the positions of the protein comprising the protein of hNGAL, AZm or 24p3 having detectable binding affinity to a given target, obtained by the method described above; (2), a fusion protein comprising the mutein of hNGAL, AZm or 24p3, where an enzyme, a protein or a protein domain, a peptide, a signal sequence and/or an affinity tag is operably fused to the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein of hNGAL, AZm or 24p3 or the fusion protein of hNGAL, AZm or 24p3 or the fusion protein of hNGAL, AZm or 24p3 or the fusion protein of hNGAL, AZm or 24p3 or the fusion protein is useful in generating or producing a mutein of hNGAL, AZm or 24p3 or the fusion protein is useful in generating or producing a mutein of hNGAL, AZm or 24p3 or the fusion protein is useful in generating or producing a mutein of the mutein with a sample suspected of containing the given target under conditions that allow complex formation between the mutein and the given target, and determining the complexed mutein by a suitable signal. The createst is a protein or protein domain, a peptide, a nucleic acid contacting the mutein may also be used in medicine, e.g. for tumour imaging cor directly for cancer therapy. The present sequence represents a condition of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocali. (NNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse 24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
Sequence
                                        exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Generating a mutein of a protein, e.g. human neutrophil gelatinase-
associated lipocalin, rat alpha2-microglobulin-related protein or mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 107-108; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24p3/uterocalin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADA00708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Skerra
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16-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-SEP-2002; 2002WO-EP010490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2003029463-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
  209 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlehuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001WO-EP011213.
2002WO-EP004223.
                               and Strep-tag II fusion proof the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "modified hNGAL 22. .199 note= "mature hNGAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprises subjecting the protein to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200. .209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "Strep-tag II affinity tag'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fusion protein"
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                                                         Matches
                                                                                    Query Match
                                                                                                                                                  The present invention relates to a method for generating muteins of huma neutrophil gelatinase-associated lipocalin (hNGAL), rat alpha2-microglobulin-related protein (A2m) or mouse 24p3/uterocalin, by subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the coat protein pill of a filamentous bacteriophage of the M13-family of or a fragment of the coat protein. The present sequence is the protein encoded by a fragment of plasmid phNGAL7, used to illustrate the invention. This sequence comprises human hNGAL, a Strep-Tag II and an invention.
                                                                                                                Sequence 258 AA;
                                                                                                                                        albumin binding domain of Protein G.
                                                                                                                                                                                                                                                                                                                                           Generating a mutein of a protein for validating the protein as drug target by subjecting the protein to mutagenesis at sequence positions corresponding to sequence positions of the human neutrophil gelatinase-associated lipocalin.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-381639/36.
N-PSDB; ADA27287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skerra A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutein; humdn; neutrophil gelatinase-associated lipocalin; hNGAL; rat; alpha2-microglobulin-related protein; A2m; mouse; 24p3; uterocalin.
                                                                                                                                                                                                                                                                                                                 Disclosure; Page 59-61; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pHNGAL7 fragment protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PIER-) PIERIS PROTEOLAB
                                                                       Local Similarity
                                                        10;
                            NHIVEPVPIDQCIDGSAWSHPQFEK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlehuber S;
                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       notes "Mature protein; fusion protein of hNGAL, Strep-
Tag II and albumin binding domain"
22. .199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "OmpA signal sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Albumin binding domain of Protein G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .258
                                                  60.7%; Score 68; DB 40.0%; Pred. No. 4.5 ative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mature hNGAL'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Strep-Tag II affinity tag
                                                                                  DB 6;
                                                        4.
                                                                                 Length 258,
                                                        Indels
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RESULT 9 ADA00702 ID ADA0

ADA00702 standard; protein; 258 AA.

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CC given target, comprising subjecting the protein to mutagenesis at CC positions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in CC muteins of the protein. Also described: (1) a mutein of hNGAL, A2m or CC 2493 having detectable binding affinity to a given target, obtained by the method described above; (2) a fusion protein comprising the mutein of CC hNGAL, A2m or 2493, where an enzyme, a protein or a protein domain, a CC peptide, a signal sequence and/or an affinity tag is operably fused to CC the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the CC comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the fusion protein of c2); and (4) a pharmaceutical composition comprising the mutein of hNGAL, A2m or 2493 or the fusion protein described above, and a carrier. The muteins have cytostatic activity, and can be used in CC gene therapy. The method is useful in generating or producing a mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein described by contacting the mutein with a sample suspected of containing the given target by contacting conditions that allow complex formation between the mutein and the given target, and determining the complexed mutein by a suitable signal. The given target is a protein or protein domain, a peptide, a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or mouse 24p3/uterocalin, comprises subjecting the protein to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutein; human neutrophil gelatinase-associated lipocalin; hNGAL; rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin; 24p3; mutagenesis; fusion protein; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocalin (hMgAL), rat alpha2-microglobulin-related protein (A2m) and a mouse 24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 98-99; 122pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADA00733.
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16-APR-2002; 2002WO-EP004223
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domain of Protein G fusion protein"
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RESULT 10
RADA27291
ID ADA27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 258 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mutein; human; neutrophil gelatinase-associated lipocalin; hNGAL; rat; alpha2-microglobulin-related protein; A2m; mouse; 24p3; uterocalin.
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                                                                                                                                           Generating a mutein of a protein for validating the protein as drug target by subjecting the protein to mutagenesis at sequence positions corresponding to sequence positions of the human neutrophil gelatinase-associated lipocalin.
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                                                                                                  Disclosure; Page 57-58; 68pp;
                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                           (PIER-) PIERIS PROTECLAB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Strep-Tag II affinity tag'
210
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Tag II and a fragment of phage
22. .199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Mature modified hNGAL"
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                                                                                                       English
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The present invention relates to a method for generating muteins neutrophil gelatinase-associated lipocalin (hNGAL), rat alpha2-microglobulin-related protein (A2m) or mouse 24p3/uterocalin, by

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Disclosure;

Page 59-61; 68pp; English.

The present invention relates

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the coat protein pIII of a filamentous bacteriophage of the M13-family of for a fragment of the coat protein. The present sequence is the protein encoded by a fragment of plasmid pHNGAL5, used to illustrate the invention. This sequence comprises human hNGAL, a Strep-Tag II and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fragment of phage coat protein pIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutein; human; neutrophil gelatinase-associated lipocalin; hNGAL; rat; alpha2-microglobulin-related protein; A2m; mouse; 24p3; uterocalin.
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                                         Generating a mutein of a protein for validating the protein as drug target by subjecting the protein to mutagenesis at sequence positions corresponding to sequence positions of the human neutrophil gelatinase-associated lipocalin.
                                                                                                 WPI; 2003-381639/36.
N-PSDB; ADA27286.
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                                                                                                                                   Skerra
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                                                                                                                                                         (PIER-) PIERIS PROTEOLAB AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                     Schlehuber S;
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                                                                                                                                                                                                                                                                                                                                                  /note= "Mature protein;
Tag II and a fragment of
22. .199
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                     'note= "Mature hNGAL"
                                                                                                                                                                                                                                                                      /note= "Amino acids 217-406
                                                                                                                                                                                                                                                                                          note= "Encoded by TAG"
                                                                                                                                                                                                                                                                                                                                                                                            note= "Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein; 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.7%; Score 68; 40.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                "Strep-Tag II affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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                                                                                                                                                                                                                                                                                                                                                             fusion function
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                                                                                                                                                                                                                                                                                                                                                             protein of hNGAL, coat protein pIII
                                                                                                                                                                                                                                                                         coat protein pIII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neutrophil gelatinase-associated lipocalin (hNGAL), rat alpha2-microglobulin-related protein (A2m) or mouse 2493/uterocalin, by subjecting the protein to mutagenesis. In the method of generating a mutein, a nucleic acid coding for the muteins of the protein resulting from mutagenesis is operably fused at the 3' end with a gene coding for the cost protein pIII of a filamentous bacteriophage of the M13-family or for a fragment of the cost protein. The present sequence is the protein encoded by a fragment of plasmid pHNCAL3, used to illustrate the invention. This sequence comprises human hNCAL, a Strep-Tag II and a fragment of phage coat protein pIII.
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Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or m
                                                                                                                                                                                                                                        27-SEP-2001; 2001WO-EP011213
16-APR-2002; 2002WO-EP004223
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                                                                                                                                             Skerra A,
                                                                                                                                                                                                                                                                                                                  18-SEP-2002; 2002WO-EP010490
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                                                                                                WPI; 2003-372000/35.
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                                                                                                                                                                                             (PIER-) PIERIS PROTEOLAB
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                                                                         ADA00731.
                                                                                                                                                Schlehuber S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "modified hNGAL, Strep
protein pIII fragment fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "amber stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "coat protein pIII fragment 217-406"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "Strep-tag II affinity tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "mature hNGAL"
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Pred. No.
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CC given target, comprising subjecting the protein to mutagenesis at C given target, comprising subjecting the protein to mutagenesis at C gostitions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in CC muteins of the protein. Also described: (1) a mutein of hNGAL, A2m or CC 2493 having detectable binding affinity to a given target, obtained by the method described above; (2) a fusion protein comprising the mutein of CC hNGAL, A2m or 2493, where an enzyme, a protein or a protein domain, a CC peptide, a signal sequence and/or an affinity tag is operably fused to the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule CC comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the fusion protein described above, and a carrier. The muteins have cytostatic activity, and can be used in CC gene therapy. The method is useful in generating or producing a mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or the fusion protein is useful in detecting a given target by contacting the mutein protein domain, a given target by contacting the mutein between the mutein and the given target and determining the complexed mutein by a suitable signal. The cc given target is a protein or protein domain, a peptide, a nucleic acid molecule, an organic molecule or a metal complex and the detection is carried out for validation of the protein as a pharmacological drug target. The mutein may also be used in medicine, e.g. for tumour imaging cor difficed hNGAL, Strep-tag II and phage coat protein piII fragment fusion protein given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocalin (hXgAL), rat alpha2-microglobulin-related protein (A2m) and a mouse 24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 94-95; 122pp; English.
Sequence 400
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밁 Ś Matches Query Match Best Local Similarity 185 NHIVFPVPIDQCIDGSAWSHPQFEK 209 10; Conservative 60.7%; Score 68; 40.0%; Pred. No. 11; Mismatches ထ 밁 6 4 Length 400 Indels 0 Gaps 0

ADA00707; ADA00707 standard; protein; 400

06-NOV-2003

(first entry)

Modified hNGAL related fusion protein SEQ ID NO:20

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XX mutein; human neutrophil gelatinase-associated lipocalin; hNGAL; rat alpha2-microglobulin-related protein; A2m; mouse 24p3/uterocalin; 24p3; mutagenesis; fusion protein; cytostatic; gene therapy; tumour imaging; cancer therapy. Region Region Protein Synthetic Peptide sapiens. /note- "modified hNGAL, Strep-tag II and phage coat protein pIII fragment fusion protein" 22. .199 /label= signal 22. .400 Location/Qualifiers note= "mature hNGAL" "Strep-tag II affinity tag

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CC given target, comprising subjecting the protein to mutagenesis at compositions 33-54, 66-83, 94-106 and/or 123-136 of hNGAL, resulting in CC muteins of the protein. Also described: (1)-a mutein of hNGAL, A2m or CC 2493 having detectable binding affinity to a given target, obtained by CC hNGAL, A2m or 2493, where an enzyme, a protein comprising the mutein of cc peptide, a signal sequence and/or an affinity tag is operably fused to CC comprising a sequence and/or an affinity tag is operably fused to CC comprising a sequence encoding the mutein of hNGAL, A2m or 2493 or the mutein of hNGAL, A2m or 2493 or the fusion protein described above, and a carrier. The muteins have cytostatic cal composition comprising CC and a carrier. The method is useful in generating or producing a mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein. The mutein of hNGAL, A2m or 2493 or a fusion protein a given target under conditions that allow complex formation between the mutein and the given conditions that allow complex formation between the mutein and the given condition is considered out for validation of the protein as a pertide, a nucleic acid condition of the protein as a pharmacological drug cor directly for cancer therapy. The present sequence represents a condition of the protein plus for tumour imaging cor directly for cancer therapy. The present sequence represents a condition of the exemplification of the protein plus invention.
                                                                                                                                                                                         Matches
                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                Sequence 400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocalin (NNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse 24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 104-105; 122pp; English.
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                                                                                   SHPQFEKXXXXXXXXXXXXXHPQFEK 26
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                                                                                                                                                                                                                          60.7%;
                                                                                                                                                                       Score 68; DB
Pred. No. 8.4;
11; Mismatches
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RESULT 14 ADA00701

ADA00701 standard; protein; 400

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ADA00701

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CC given target, comprising subjecting the protein to mutagenesis at CC given target, comprising subjecting the protein to mutagenesis at CC muteline of the protein. Also described: (1) a muteline of hNGAL, A2m or CC 2493 having detectable binding affinity to a given target, obtained by the method described above; (2) a fusion protein comprising the mutein of NGAL, A2m or CC peptide, a signal sequence and/or an affinity tag is operably fused to CC the amino or carboxy terminus of the mutein; (3) a nucleic acid molecule comprising a sequence encoding the mutein of hNGAL, A2m or 24p3 or the fusion protein described above, CC the mutein of hNGAL, A2m or 24p3 or the fusion protein described above, CC and a carrier. The muteins have cytostatic activity, and can be used in CC gene therapy. The method is useful in generating or producing a mutein of hNGAL, A2m or 24p3 or the fusion protein mutein of the suspection of the mutein of hNGAL, A2m or 24p3 or the fusion protein target by contacting the mutein of the mutein of hNGAL, A2m or 24p3 or the fusion protein. The mutein of the suspected of containing the given target under CC conditions that allow complex formation between the mutein and the given carget, and determining the complexed mutein by a suitable signal. The given target is a protein or protein domain, a peptide, a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a method for generating a mutein of a protein selected from a human neutrophil gelatinase-associated lipocalir (hNGAL), rat alpha2-microglobulin-related protein (A2m) and a mouse 24p3/uterocalin (24p3), where the mutein has a detectable affinity to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generating a mutein of a protein, e.g. human neutrophil gelatinase-associated lipocalin, rat alpha2-microglobulin-related protein or m 24p3/uterocalin, comprises subjecting the protein to mutagenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 96-98; 122pp; English.
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16-APR-2002; 2002WO-EP004223.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PIER-) PIERIS PROTEOLAB
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protein pIII fragment fusion protein"
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Sequence 400 AA;

molecule, an organic molecule or a metal complex and the detection is carried out for validation of the protein as a pharmacological drug target. The mutein may also be defined in medicine, e.g. for tuneour imaging or directly for cancer therapy. The present sequence represents a modified hNGAL, Strep-tag II and phage coat protein pIII fragment fusion protein given in the exemplification of the present invention.

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RESULT 15
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The invention relates to a novel isolated, modified ADAMTS4 (a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif 4) protein this improved stability compared to a naturally occurring, full-length ADAMTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAMTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc
                                                                                                      New isolated, modified ADAMTS4 (aggrecanase) stability useful for identifying inhibitors treating aggrecanase-associated conditions,
                                                                                                                                                                                                                                                                                                                                                            29-JUL-2003; 2003WO-US023484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human aggrecanase modified
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                                                                                  Claim
                                                                                                                                                        WPI; 2004-143860/14.
                                                                                                                                                                                         Corcoran CJ,
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) MCDONAGH T.
) FREEMAN B A.
GEORGIADIS K E
LAVALLIE E R.
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                                                                                 SEQ ID NO 49; 117pp; English.
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Georgiadis KE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein;
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Lavallie
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Pred. No.
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ie ER;
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                                                                                                       ) protein with improved of the enzyme activity for including osteoarthritis.
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                                                                                 Query Match
Best Local
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                                                                                                                                                                                    metalloproteases and include aggrecanases amongst their members. The protein of the invention demonstrates osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rhe courrent sequence arthritis, periodontal disease and Crohn's disease. The current sequence is that of a human aggrecanase modified ADAMTS4 (mTS4) protein of the
                                                                                                                                     Sequence 646 AA;
                                                                                                                                                                       invention.
615
                                                                  10;
                                  1 WSHPQ----FEKXXXXXXXXXXXXXSHPQFEK 26
                                                                                  Similarity
WLHRRAQILEILRRRPWAGRKGSAWSHPQFEK 646
                                                                    Conservative
                                                                                  58.9%;
                                                                    12;
                                                                                  Score 66;
Pred. No.
                                                                    Mismatches
                                                                                      31;
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Search completed: March Job time : 118.106 secs 'n 2005, 13:02:50

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

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Minimum DB seq length: 0
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Published Applications AA:*

1: /cgn2 6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2 6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/US06_NEW PUB.pep:*

4: /cgn2 6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2 6/ptodata/2/pubpaa/US07_NEW PUB.pep:*

6: /cgn2 6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7: /cgn2 6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

8: /cgn2 6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

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/ Cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
/ Cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 2 3 4 4 4 4 7 7 7 10 11 11 11 11 11 11 11 11 11 11 11 11	No.
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Sequence 3, Appli Sequence 10, Appl Sequence 11, Appli Sequence 4, Appli Sequence 49, Appl Sequence 27, Appl Sequence 27, Appl Sequence 24, Appl Sequence 31, Appl Sequence 31, Appl Sequence 34, Appl Sequence 34, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	Description

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Sequence 2199, Ap	0 10407	ס פ	10406	e 51780			169	39,	40,	15,	e 8,	e 6,	e 12, App	e 11,	e 10,	Sequence 9, Appli	e 8,	e 7, Appl	ი ა	e 4, Appl	8, Appl	e 12, App	u	30,	e 53, Ap	e 1105,	e 1103,	Φ	Sequence 851, App	4.

## ALIGNMENTS

RESULT 1 US-10-026-578B-3

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Sequence 3, Application US/10026578B
Publication No. US20030083474A1
GENERAL INFORMATION:
APPLICANT: Semindt. Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
PILE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFREENCE: 100810.01US1
CURRENT FILING DATE: US/10/026,578B
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR PILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE: PRT
ORGANISM: Artificial sequence
FEATURE: NAME/KEY: MISC FEATURE
INCORTION: (0): -[9]
IOCATION: (0): -[9]
IOCATION: (10): (10)
IOTHER INFORMATION: X represents a single amino acid at the position indicated
FEATURE: NAME/KEY: MISC FEATURE
INCORMATION: X represents a single amino acid at the position indicated
FEATURE: NAME/KEY: MISC FEATURE
INCORTION: (11): (11)
IOTHER INFORMATION: X represents a single amino acid at the position indicated
FEATURE: NAME/KEY: MISC FEATURE
INCORTION: (11): (11)
IOTHER INFORMATION: X represents a single amino acid at the position indicated
FEATURE: NAME/KEY: MISC FEATURE
INCORTION: (11): (11)
IOTHER INFORMATION: X represents a single amino acid at the position indicated
FEATURE: NAME/KEY: MISC FEATURE
INCORTION: (12): (13): (14)
INCORTION: (13): (14)
INCORDANTION: X represents a single amino acid at the position indicated
FEATURE:
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US-10-026-578B-10
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                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: POSEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/10026578B Publication No. US20030083474A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/026,578B CURRENT FILING DATE: 2002-11-11 PRIOR APPLICATION NUMBER: DE 101 13 776.1 PRIOR FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: PCT/EP01/11846 PRIOR APPLICATION NUMBER: PCT/EP01/11846 PRIOR FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                            LOCATION: (9)...(28) OTHER INFORMATION: X represents a single amino acid at each of the positions indicat OTHER INFORMATION: ed; some of the amino acids may be missing. Where amino acids are OTHER INFORMATION: missing, the total numbers of x will be no less than 5
                                                                                                                              NAME/KEY: misc_feature
OTHER INFORMATTON: Artificial Sequence represents peptide binding module
                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                              NAME/KEY: MISC_FEATURE
                                                                                                                                                                                                                                                                                                                                                                              ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
OTHER INFORMATION: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: X represents a single amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC FEATURE
LOCATION: (14) . (14)
OTHER INFORMATION: X represents a single amino
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                                                                          Local Similarity
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                    1 WSHPQFEK--
                                                       26; Conservative
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92.3%;
                                                                      86.6%;
-XXXXXXXXXXWSHPQFEK 26
                                                  Score 97; DB 1
Pred. No. 7.2e
0; Mismatches
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Pred. No.
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2.4e-05;
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7.2e-05;
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                                                                                     Length 36;
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                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10026578B Publication No. US20030083474A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1 SEQ ID NO 11
                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/026,578B CURRENT FILING DATE: 2002-11-11 PRIOR APPLICATION NUMBER: DE 101 13 776.1 PRIOR FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: PCT/EP01/11846 PRIOR FILING DATE: 2001-10-12
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Publication No.
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: IBA (GmbH)
APPLICANT: Schmidt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/026,578B CURRENT FILING DATE: 2002-11-11 PRIOR APPLICATION NUMBER: DE 101 13 776.1 PRIOR FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: PCT/EP01/11846 PRIOR FILING DATE: 2001-10-12
                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as
FILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: IBA (GmbH)
APPLICANT: Schmidt,
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: X represents a single amino acid at the position indicated
                                                                         FEATURE:
OTHER INFORMATION: Synthetic Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                       FEATURE:
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OTHER INFORMATION: Artificial
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                                                                                                                                                                        ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: MISC_FEATURE LOCATION: (9)..(28)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetic Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Of the five repeats may
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Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GGGS) repeats between position 9 be missing. However, at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide binding
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RESULT 5

US-10-628-432-49

; Sequence 49, Application US/10628432

; Publication No. US20040142863A1

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
US-10-026-578B-4
                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                            Matches
APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: MISC_FEATURE
LOCATION: (24)..(24)
OTHER INFORMATION: X represents a single
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LOCATION: (23)...(23)
OTHER_INFORMATION: X represents a single
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LOCATION: (17) ... (17)
OTHER INFORMATION: X represents a single amino
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LOCATION: (14) ... (14)
OTHER INFORMATION: X represents
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LOCATION: (13)..(13)
OTHER_INFORMATION: X represents
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OTHER INFORMATION: X represents a single amino
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OTHER INFORMATION: X represents a single amino
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OTHER INFORMATION: X represents
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OTHER INFORMATION: X represents
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                                                                                                                                                                                               WSHPQFEXXXXXXXXXXXXXXX -- HPQ 21
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                       62.5%;
91.3%;
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Pred. No.
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Mismatches
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RESULT 6
US-10-628-432-27
; Sequence 27, Application US/10628432
; Publication No. US20040142863A1
; GENERAL INFORMATION:
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                                                                                                                  ; OTHER INFORMATION: furin-processed construct US-10-628-432-47
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Best Local S
Matches 10
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TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: M101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 49
LENGTH: 646
TYPE: PRT
ORGANISM: Artificial
FEATURE:
FEATURE:
OTHER INFORMATION: furin-processed construct
                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1 SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                              Sequence 47, Application US/10628432 Publication No. US20040142863A1 GENERAL INFORMATION:
                                                                 Query Match
Best Local Similarity
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Matches 10; Conserv
                                                                                                                                                                                                                                           TITLE OF INVENTION: Modified ADAMTS4 molecules FILE REFERENCE: AM101378 CURRENT APPLICATION NUMBER: US/10/628,432 CURRENT FILING DATE: 2003-07-29 NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wyeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: modified ADAMTS4 molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                ENGTH: 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   827 WLHRRAQILEILRRPWAGRKGSAWSHPQFEK 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WSHPQ-----FEKXXXXXXXXXXXXXSHPQFEK 26
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SHPQFEK-----XXXXXXXXXXXXWSHPQFEK 26
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                                                   Conservative
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                                                               57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.9%; Score 66; DB 31.2%; Pred. No. 42; tive 12; Mismatches
                                                 Score 64.5; D
Pred. No. 32;
12; Mismatches
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2; Mismatches
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SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 485

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Sequence 24, Application US/10628432

Publication No. US20040142863A1

GENERAL INFORMATION:
APPLICANT: Wyeth
ITILE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378

CURRENT APPLICATION NUMBER: US/10/628,432

CURRENT FILING DATE: 2003-07-29

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.1

SEQ ID NO 24

I ENGREY: 607
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; OTHER INFORMATION: Truncated ADAMTS4 molecule
US-10-628-432-24
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                                                                                       RESULT 10
US-09-809-517A-34
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                                                                                                                                                                                                                                                                                                          , OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-809-517A-31
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Lohning, Corinna
APPLICANT: Lohning, Corinna
ITTLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT PILING: DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING: DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING: DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
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Best Local :
                                                                                                                                                                                                                         Query Match
Best Local Similarity 41.7
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/09809517A Patent No. US20020034733A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 11;
                               Sequence 34, Application Usanent No. US20020034733A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 31
LENGTH: 24
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733Alel methods for displaying (poly)peptides/prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial sequence
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| SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 697
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                                                                     Application US/09809517A
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Pred. No. 50;
                                                                                                                                                                                                                                                            Score 64; DB 9
Pred. No. 0.82;
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CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 9914072.4
PRIOR RILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
VNUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-34
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                                                                                                                       US-10-887-228A-9
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Best Local Similarity
Conserv
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Sequence 9, Application US/10887228A
Publication No. US20050037402A1
GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: Device and Process for Direct Qu
TITLE OF INVENTION: Substance That is Contained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 245
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Device and Process for Direct Quantitative in vitro TITLE OF INVENTION: Substance That is Contained in a Sample FILE REFERENCE: $30569US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: artificial
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Pred. No.
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FILE REFERENCE: S30569US
FILE REFERENCE: S30569US
CURRENT APPLICATION NUMBER: US/10/887,228A
CURRENT FLING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: DE 103 31 093.2

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RESULT 14
US-10-408-765A-434
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                                                                                                                                                                                          Sequence 434, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
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Publication No. US20050037402A1
GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: Device and Process for Direct Quantitative in vitro Determination TITLE OF INVENTION: Substance That is Contained in a Sample
FILE REFERENCE: S30569US
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PRIOR APPLICATION NUMBER: US 60/478,262
PRIOR FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
SEQ ID NO 9
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SEQ ID NO 5
LENGTH: 252
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APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TRAGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/887,228A CURRENT FILING DATE: 2004-07-09 PRIOR APPLICATION NUMBER: DE 103 31 093.2 PRIOR FILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: US 60/478,262 PRIOR FILING DATE: 2003-07-16 NUMBER OF SEQ ID NOS: 12
                                                                                                                               APPLICANT:
                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE: OTHER INFORMATION: Fab fragment of variable heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: artificial
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                                                                                                                             Gibson, Bradford W.
Taylor, Steven W.
Glenn, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.1%; Score 64; DB 41.7%; Pred. No. 16; ative 12; Mismatches
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RESULT 15
US-10-741-600-851
; Sequence 851, Applicat
; publication No. US2000;
; GENERAL INFORMATION:
Search completed: March Job time: 80.8537 secs
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                                                                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-741-600-851
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DET
FILE REFERENCE: CL001499
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SOFTWARE: FASTSEQ for Windows Version 4.0.
SEQ ID NO 851
                                                                                                                                                 Query Match 57.1%; Score 64; DB Best Local Similarity 37.5%; Pred. No. 59; Matches 9; Conservative 10; Mismatches
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Best Local Similarity 37.5%;
Matches 9; Conservative 10
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 434
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                  LENGTH: 699
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Pred. No. 59;
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Result
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Maximum DB
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Maximum Match 100%
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Perfect score:
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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| cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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       US-09-809-517A-31
US-09-809-517A-34
US-09-809-517A-30
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US-09-977-137A-7
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Sequence 31, Appl
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Corinna No. 6753136e Particles v PHO/11 PHO/11 NUMBER: US/0 NUMBER: US/0 NUMBER: EP 991 NUMBER: EP 991 NUMBER: EP 991	CXXXXX	57. 41. ive	l sequence Description	Corinna Corinna Corinna Corinna No 675 Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Partic Parti		2123 2324 3070 3088 3110 3110 31110 31111 31111 31111 8 8 8 8
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09809517A  3136el methods for displaying les via disulfide bonds  US/9/809,517A 03-15 03-15 10-0107551-8	QPEKXXXXXXXXXXXXXSHPQFEK 26 :  : :::::::         EPEQKLISEEDLNGAPWSHPQFEK 24	Score 64; DB 4; Length 2 Pred. No. 0.073; 12; Mismatches 0; Indel	of Artificial Sequence:	US/09809517A  inna 6753136el methods for displaying rticles via disulfide bonds 1  3ER: US/09/809,517A  3D1-03-15 101-03-15 1: EP 99114072.4 107-20 12: EP 00103551.8 102-18	ALIGNMENTS	US-09-949-016-7517 US-09-902-540-9732 US-09-961-403-7 US-09-562-702A-8 US-09-562-702A-2 US-09-562-702A-6 US-09-562-702A-6 US-09-562-702A-6 US-09-562-702A-7 US-09-17-254-86 US-09-917-254-86 US-09-917-254-86 US-09-949-016-5937 US-08-46-309-4 US-08-46-309-7 US-08-46-309-7 US-08-948-097-2 US-09-382-7368-8 US-09-382-7368-8 US-09-382-7368-8 US-09-619-103-9 US-101-104-218-5 US-09-809-517A-9
(poly) peptides/proteins		24; ls 2; Gaps 1;	synthetic module	(poly)peptides/proteins		Sequence 7517, Apsequence 9732, Apsequence 7, Appli Sequence 7, Appli Sequence 4, Appli Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 8, Appli Sequence 937, Appli Sequence 937, Appli Sequence 4, Appli Sequence 4, Appli Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli
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PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR FILING DATE: 2000-02-18 NUMBER OF SEQ ID NOS: 41

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US-09-809-517A-34
                   OI Das
                                          APPLICANT LORING, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Patent No. 6753136
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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SOFTWARE: CuraPatSeqFormatter Version
SEQ ID NO 995
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SOFTWARE: PatentIn version 3.0 SEQ ID NO 30 LENGTH: 21
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Best Local :
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CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
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APPLICANT: Mansfield,
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NAME/KEY: misc_feature
LOCATION: (0)...(0)
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ORGANISM: Homo sapiens
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41.7%; Pred. No. 0.077;
Live 12; Mismatches
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Pred. No.
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; OTHER INFORMATION: Description of Artificial Sequence: US-09-977-137A-4
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US-09-809-517A-33
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                                                                                                   FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                          Sequence 4, Applicati
Patent No. 6750042
GENERAL INFORMATION:
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SEQ ID NO 33
LENGTH: 22
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TITLE OF INVENTION: No. 6753136el methods for displaying (poly) peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: NORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR PILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
NUMBER OF SEQ ID NOS: 41
NUMBER OF SEQ ID NOS: 41
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APPLICANT: Lohning,
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Appl. Patent No. 675313
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                                               ORGANISM: Artificial Sequence
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                                  FEATURE:
                                                                        TYPE: PRT
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44.4%; Pred. No. 0
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATCHIT Ver. 2.0
SEQ ID NO 5
LENGTH: 117:
TYPE: PRT
TYPE: PRT
TYPE: PRT
CENTRE: 17:
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US-09-977-137A-7
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Methal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION UNMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 117
TYPE: PRT
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Matches
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Best Local
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APPLICANT: Caguiat, Jonathan
TITLE OP INVENTION: Metal Binding Proteins,
TITLE OP INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                               -09-977-137A-7
                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:
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Similarity 44.4%;
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                                                              Conservative
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 117
TYPE: PRT
                                  RESULT 11
US-09-977-137A-10
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US-09-977-137A-9
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FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEC. TO TO THE PRIOR FILING DATE: 2000-10-12
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Patent No. 6750042
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
Sequence 10, Application US/09977137A Patent No. 6750042
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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TYPE: PRT
ORGANISM: Artificial Sequence
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44.4%; Pred. No.
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RESULT 13
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US-09-977-137A-11
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US-09-977-137A-10
                                                                                                   GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonath
                                                                                                                                                          Sequence 12, Application US/09977137A Patent No. 6750042
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Best Local Similarity
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SEQ ID NO 11
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Patent No. 67500
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CURRENT APPLICATION NUMBER: US/09/977,137A CURRENT FILING DATE: 2001-10-12
                                                      APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding
TITLE OF INVENTION: Methods
                                          FILE REFERENCE: 79-00
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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APPLICANT: Caguiat, Jonati
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
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ORGANISM: Artificial Sequence
FEATURE:
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PRIOR FILING DATE: 2000-10-12
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
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Pred. No. 1.9;
                                                                           Proteins, Recombinant Host Cells and
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RESULT 15
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                                                                                                                                                                                                                                              Patent No. 5814502
                                                                                                                                                                                                                                                            Sequence 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Applicat Patent No. 6750042 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-10-1
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRICE APPLICATION NUMBER: US 60/240,465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT . ORGANISM: Artificial Sequence
                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center/Patent Division
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                                                                                                                                               TITLE OF INVENTION:
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ZIP: 46285
COMPUTER READABLE FORM:
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                            COUNTRY:
                                                               CITY: Indianapolis
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                                                                                                                          Otto, Keith A.

Rao, Ramachandra N.

RVENTION: FUSION PROTEINS COMPRISING CELL CYCLE

NVENTION: REGULATORY PROTEINS
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44.4%; Pred. No. 1.9;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Copyright (c) 1993 - 2005
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C;Genetics:
A;Gene: pAiGO
C;Superfamily: membrane-bound alcohol dehydrogenase, cytochrome c sub
C;Superfamily: membrane-bound alcohol dehydrogenase, cytochrome c sub
C;Keywords: chromoprotein; heme; iron; metalloprotein
F;58,61/Binding site: heme (Cys) (covalent) #status predicted
F;62/Binding site: heme iron (His) (axial ligand) #status predicted
F;204,207/Binding site: heme (Cys) (covalent) #status predicted
F;208/Binding site: heme iron (His) (axial ligand) #status predicted
F;336,339/Binding site: heme iron (His) (axial ligand) #status predicted
F;340/Binding site: heme iron (His) (axial ligand) #status predicted
hypothetical protein F2G19.1 [imported] - Arabidopsis thaliana (c)Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96510
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83444
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Li.; Lory, S.; Olson, M.V.
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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A; Residues: 1-433 <STO>
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C;Species: Pseudomonas aeruginosa
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Best Local
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Pred. No. 8
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glass iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia co A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                   unknown protein encoded within prophage CP-933U [imported] - Escherichia coli C;Species: Escherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
A85821
                                                                                  A;Cross-references: UNIPROT:Q8X4V0; GB:AE005174; NID:g12516136; PIDN:AAG57029.1; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-103 <STO>
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R;Perna, N.T.; Plun
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A; Residues: 1-103 <HAY>
A; Cross-references: UNIPROT: Q8X4V0; GB: BA000007;
A; Experimental source: strain O157:H7, substrain
C; Genetics:
A; Gene: ECs2757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Igasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7

A;Reference number: A99629; MUID:21156231; PMID:11258796
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E90973
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q9C642; GB:AE005173; NID:g11321777; PIDN:AAG34254.1; GSPDB:G
C;Genetics:
C;Genetics: A;Gene: F2G19.1
A;Gene: F2G19.1
A;Map position: 1
C;Superfamily: tomato DCL protein
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E90973
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A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C96510
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Best Local S
Matches 6
  Best Local
                    Query Match
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8; Conserv
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51.3%;
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Score
Pred.
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Pred. No. 7
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RIMD 0509952
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RESULT 7
A54660
histidine rich calcium binding protein - human
C;Species: Homo sapiens (man)
C;Species: 02-Unr.1995 #sequence_revision 02-Jun-1995 #text_change
C;Accession: A54660
C;Accession: A5460
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A;Residues: 1-103 <HAY>
A;Experimental source: strain O157:H7, substrain RIMD 0509952
A;Genetics:
A;Gene: ECs2201
                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ECs2201 [imported] - Escherichia coli (strain O157:H7, subs C/Species: Escherichia coli
C/Species: Escherichia coli
C/Species: Bscherichia coli
C/Species: Bscherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: A90904
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; H
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A99529; MUID:21156231; PMID:11258796
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A;Nolecule type: DNA
A;Residues: 1-103 <STO>
A;Cross-references: UNIPROT:Q8X549; GB:AE005174;
A;Cross-references: strain O157:H7, substrain
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C85713
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A;Accession: C85713
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A; Reference number: A85480; MUID:21074935; PMID:11206551
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R;Perna, N.T.; Pluni
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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L4; Mismatches
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Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrain
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R;Hofmann, s

Topham, M.; Hsieh, C.L.; Francke,

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09-Jul-2004

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hypothetical 24.1K protein - Neurospora crassa
C;Species: Neurospora crassa
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-242 <LYN>
A;Cross-references: UNIPROT:O59743; EMBL;AL023634; PIDN:CAA19173.1; GSPDB:GN00067; SPDB
A;Experimental source: strain 972h-; cosmid c530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, submitted to the EMBL Data Library, May 1998
A;Reference number: Z21934
A;Accession: T40523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein SPBC530.07c - fission yeast (Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
T40523
ફ
                      Query Match
Best Local Similarity
Watches 6; Conserve
                                                                                                                         A;Experimental source: strain OR23-IV-A
A;Note: translation of the nucleotide sequence is not complete
C;Superfamily: Neurospora crassa hypothetical 24.1K protein
                                                                                                                                                                                                                                                      Gene 88, 159-165, 1990
A;Title: Characterization of telomere DNA from Neurospora crassa
A;Reference number: JH0145; MUID:90269603; PMID:1971801
A;Accession: JH0145
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A;Map position: 19q13.3-19q13.3
C;Keywords: calcium binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-699 < HOF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Reference number:
A, Accession: A54660
                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-207 <SCH>
                                                                                                                                                                                                                                                                                                                                            R;Schechtman, M.G.
                                                                                                                                                                                                                                                                                                                                                              C; Accession: JH0145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P23327; GB:M60052; NID:g183918; PIDN:AAA88071.1; PID:g18391
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Best Local S
Matches 9
                                                                                                                                                                                        Cross-references: UNIPROT:Q01400; GB:M37064; NID:g168912; PIDN:AAC13656.1; PID:g529468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: T40523
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: SPDB:SPBC530.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 30.4%; Score 56; es 7; Conservative 77.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA and genomic cloning of HRC, a human sarcoplasmic reticulum protein, and lonce number: A54660; MUID:91244309; PMID:2037293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFQKNCPEEMEFVKWWGQPSFGK 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HPD-ENKDVSTENGHHFWSHPDREK 90
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  FEKXXXXXXXXXXXXXHPQF 25
                                            Conservative
                                       48.7%; Score 55; DB
30.0%; Pred. No. 26;
htive 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OMIM: 142705
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                                                                                  Length 207;
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                                          Indels
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RESULT 11
T22847
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                                                                                                                                                                                                                                                                           A; MOLECULA: -I. 1087 <WILDARD A; Cross-references: UNIPROT: Q20948;
A; Cross-references: Clone F57C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Keddie, J.S.; Carroll, B.; Jones, J.D.G.; Gruissem, W.
EMBO J. 15, 4208-4217, 1996
A;Title: The DCL gene of tomato is required for chloroplast development and palisade cel
A;Reference number: S71748; MUID:97015121; PMID:8861949
A;Accession: S71749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DCL protein precursor, chloroplast - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
                                                                                                                                    A;Introns: 262/3; 351/3; 391/3; 627/3; F;307-364/Domain: bromodomain homology F;579-636/Domain: bromodomain homology
                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A;Reference number: Z19625
A;Accession: T22847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F57C7.1b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004 C;Accession: T22847
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A;Experimental source: strain Moneymaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-224 < KEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:Q42463; EMBL:U55278; NID:g1323697; PID:g1323698
A;Experimental source: strain Moneymaker
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S71749; S71748
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                                                                                                                                                                                                           A; Map position:
                                                                                                                                                                                                                                    A; Gene: CESP:F57C7.1b
                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 128/2; 166/3
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                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                             Genetics:
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Conservative
                                              Conservative
                                                                  48.2%;
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                                            15;
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Pred. No. 28;
13; Mismatches
                                                                  Score 54.5; DB 2;
Pred. No. 2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                  February 1996
                                                                                                                                                                                                                                                                                                         EMBL: Z69646; PIDN: CAA93475.1; GSPDB: GN00028; CESP: F5
                                              Mismatches
                                                                                                                                                               795/2;
<BRO1>
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                                                                                      Length 1087;
                                              Indels
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                                              Gaps
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probable calnexin - Jerusalem artichoke (;Species: Helianthus tuberosus (Jerusalem artichok C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T10892 R;Hasenfratz, M.; Jeltsch, J.; Lesot, A.; Michalak, R;Hasenfratz, M.; Jeltsch, J.; Lesot, A.; Michalak,
                                                                                                                                RESULT 14
T10892
        submitted
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                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: this accession replaces an interim accession for a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000, MUID:98344137; PMID:9679194
A;Accession: B71058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
B71058
                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: PH1160
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:O58874; GB:AP000005; NID:g3236132; PIDN:BAA30260.1; A;Experimental source: strain OT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-211 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
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C;Species: Pyrococcus horikoshii
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A;Molecule type: DNA
A;Residues: 1-1250 <WIL
A;Cross-references: UNIPROT:Q20947;
A;Experimental source: clone F57C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F57C7.1a - C
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
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                                                                                                                                                                                                                                                                                                 Matches
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;Introns: 262/3; 351/3; 391/3; 431/3; 667/3;
;307-364/Domain: bromodomain homology <BRO1>
;619-676/Domain: bromodomain homology <BRO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; nucleic acid sequence not shown; translation
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Gene: CESP:F57C7.la
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8; Conserv
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    Jeltsch,
EMBL Data
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                                                                                                                                                                                                                                                                                                                 47.8%; Score 54; DB 31.0%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.2%; Score 54.5; DB 2;
22.9%; Pred. No. 2.5e+02;
tive 15; Mismatches 3;
J.; Lesot, A.; Michalak, M.;
Library, July 1994
                                                                                  (Jerusalem artichoke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans
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RESULT 15
I49281
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(;Superfamily: disintegrin homology F;246-326/Domain: disintegrin homology F;180/Active site: Glu #status predicte
                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 1-600 <RES>
A;Cross-references: EMBL:U22056; NID:g965009; PIDN:AAA74920.1; PID:g965010
C;Genetics:
                                                                                                                                                                                                                                                                                                                                            C;Accession: 149281
R;Wolfsberg, T.G.; Straight, P.D.; Gerena, R.L.; Huovila, A.P.; Primakoff, Dev. Biol. 169, 378-383, 1995
A;Title: ADAM, a widely distributed and developmentally regulated gene family, Reference number: 148100; MUID:95269891; PMID:7750654
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                                                                                                                                                                                                                                                                                                                                                                                                                                              fertilin alpha precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-U1-1996 #sequence_revision 02-Uul-1996 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: ER-bound chaperone C;Superfamily: calnexin C;Keywords: endoplasmic reticulum; molecular chaperone
                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Modecule type: mRNA
A;Residues: 1-540 <HAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: Cloning and characterization of a cDNA encoding an analog A;Reference number: 217201
A;Reference number: 217201
A;Accession: 710892
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                 Matches
                                                                                                 Query Match
Best Local
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                                     SHPPRSRKPDDLLVLTDWWSHTKY
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25.0%; Pred. No. 1.26
Live 14; Mismatches
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Listing first 45 s
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137.824 Million cell updates/sec
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1: uniprot_sprot:*
2: uniprot_trembl:*
   GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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SRCH HUMAN

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                                                                                                                                                                                                                                                                                                          06z315 oryza sativ
08cjd2 rattus norv
08ch90 rattus norv
09i3c1 pseudomonas
08rv8 coffea arab
09c642 arabidopsis
09ad61 streptomyce
062tr3 bacillus li
08x549 escherichia
08x4v0 escherichia
08x4v0 pseudomonas
 Q7us12
Q8nf12
Q8nf12
Q6eq72
Q75c03
Q9p4u2
Q8wkk9
Q8wbk90
Q9bb93
Q9bb93
Q8pd974
Q8gq74
Q8gq74
Q8gn18
Q8gn18
Q8gn16
Q8tc236
                                                                                                                                                                                                                                           Q6vs51
Q8xnd2
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2 pleurotus n
2 rhodopirell
7 bacteroides
                                                                                                                                                                                                                                                                           1 pseudomonas
8 coffea arab
2 arabidopsis
1 streptomyce
3 bacillus li
2 bacillus li
2 escherichia
9 escherichia
0 escherichia
1 influenza a
2 clostridium
 a ashbya goss
phycomyces
marathrum s
vanroyenell
soserya coul
pseudomonas
bradyrhizob
sutilago ma
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suspien
coxiella bu
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oryza sativ
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Q6Z315
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Regult No.

Database

<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	33	32
55.5	56	56	56	56	56	56	56	56	56	56	56	56	56
49.1						49.6				49.6		49.6	49.6
1749	2547	809	372	372	348	331	313	296	270	242	239	211	183
10	μ	N	N	N	N	N	N	N	N	N	N	N	i
Q8T0W6	FAFX HUMAN	Q910A3	Q8MK10	Q8MK09	Q6LYA4	Q67PX1	Q9N4A7	Q8PHM1	Q9BLU4	059743	Q6LV35	Q9N4A6	Q6D2A5
Q8t0w6	Q93008	Q910a3	Q8mk10	Q8mk09	Q6lya4	Q67px1	Q9n4a7	Q8phm1	Q9blu4	059743	Q61v35	Q9n4a6	Q6d2a5
echinococcu	h probable	cyprinus ca	macaca mula	macaca mula	methanococc	symbiobacte	caenorhabdi	xanthomonas	leishmania	schizosacch	photobacter	caenorhabdi	erwinia car

# ALIGNMENTS

Searched:

Sequence:

Run on:

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QBCJD2; 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25	3 HPQFEKXXXXXXXXXXXXWSHPQFE 26    :  :::::::  :   30 HPQYEKXIGCGIDYLTVGLHPEFE 53  1TT 2 1D2 1D2 1D2 1D3 1D4 1D5 1D5 1D5 1D5 1D5 1D5 1D6 1D5 1D6 1D7 1D7 1D7 1D8 1D8 1D8 1D8 1D8 1D8 1D8 1D8 1D8 1D8	SEQUENCE FROM N.A.  Sabaki T., Matsumoto T., Yamamoto K.;  Sabaki T., Matsumoto T., Yamamoto K.;  Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.  SUBMI; AP005287; BAD17315.1;  EMBL; AP004817; BAD17127.1;  SEQUENCE 107 AA; 12839 MW; 00F06AF3A12B0EB1 CRC64;  SEQUENCE 107 AA; 12839 MW; 00F06AF3A12B0EB1 CRC64;  SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER SUBMITTER S	All.16-2; Synonyms=P( All.16-2; Synonyms=P( a (japonica cultivar-c Viridiplantae; Strept ta; Magnoliophyta; Lil ae; Oryzeae; Oryza. 39947; OM N.A. MAK-2002) to the EMBL/	Q6Z315 PRELIMINARY; PRT; 107 AA. Q6Z315; Q5.JUL-2004 (TrEMBLrel. 27, Created) O5.JUL-2004 (TrEMBLrel. 27, Last sequence update) O5.JUL-2004 (TrEMBLrel. 27, Last annotation update)

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Best Local S
Matches 8
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O913C1;
O1-MAR-2001 (TEMBLES 16, C
01-MAR-2001 (TEMBLES 16, L
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Nakamura I., Yao Y., Suzuki N.;

Nakamura I., Yao Y., Suzuki N.;

Submitted (DEC-2002) to the EMBL/GenBank/DDB.

EMBL; AB097860; BAC44887.1; -.

HSSP; P30803; 1AZS.

GO; GO:0004383; F:guanylate cyclase activity

GO; GO:0016829; F:lyase activity; IEA.

GO; GO:0007242; P:intracellular signaling can

InterPro; IPR00154; G cyclase.

InterPro; IPR00154; G:RNAeyn la bind.

Pfam; PF00211; Guanylate cyc; 1.

SMART; SM00044; CYCG; 1.

SMART; SM00044; CYCG; 1.
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Best Local :
                          NCBI_TaxID=287;
                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae; Pseudomonas.
                                                                                             Pseudomonas aeruginosa.
                                                                                                                  OrderedLocusNames=PA1600;
                                                                                                                                        01-MAR-2001 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
Probable cytochrome c.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Soluble guanylyl cyclase alpha 2 subunit E219G muta
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GO; GO:007242; P:intracellular signaling cascade;
InterPro; IPR001054; G cyclase.
Piam; PF00211; Guanylate_cyc; 1.
SMART; SM00044; CYCC; 1.
SMART; SM00044; CYCC; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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Last
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EMBL/GenBank/DDBJ databases.
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Pred. No.
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Pred. No. 15;
L1; Mismatches
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Sciurognathi; Muridae; Murinae; Rattus.
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RESULT 6
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Q9C642
Q9C642;
01-JUN-2001
01-JUN-2001
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01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                         Marraccini P., Meunier A.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AJ420083; CAD12248.1; -
                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; aster lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae; Coffeea.
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Name=dcl;
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043; DOI=10.1038/35023079;

MEDLINE-20437337; PubMed=10984043; DOI=10.1038/35023079;

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InterPro; IPR003345; CytC_heme_BS.
InterPro; IPR009056; Cytochrome_c.
InterPro; IPR00308B; Cyt_CI.
Pfam; PF00034; Cytochrom_C; 2.
ProDom; PD011584; CytC_adh; 2.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_3.
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EMBL; AY128277; AAM91086.1; -.
EMBL; BY014877; AAM91860.1; -.
PIR; C96510; C96510
SEQUENCE 219 AA; 25448 MW; C
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01-JUN-2001
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
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01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein SCP1.89c.
OrderedLocusNames=SCP1.89c;
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Eukaryota; Viridiplantas; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyeledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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"Complete genome sequence coelicolor A3(2).";
Nature 417:141-147(2002).
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Tang M., de Leon A.L., Xiang H., Gusti V., Clausen I.G.,
Rasmussen M.D., Andersen J.T., Jorgensen P.L., Larsen T.:
Sorokin A., Bolotin A., Lapidus A., Galleron N., Ehrlich
Berka R.M.;
Veith B., Herzberg C., Steckel S., Feesche J., Maurer K.H., Ehrenzeich P., Baeumer S., Henne A., Liesegang H., Merkl R., Ehrenzeich A., Gottschalk G.; "The Complete Genome Sequence of Bacillus licheniformis DSM13, Organism with Great Industrial Potential."; J. Mol. Microbiol. Biotechnol. 7:204-211(2004).
                                                                                                                                                                                                                                                                                                                                                                           Name=ypiP; ORFNames=BLi02322;
Bacillus licheniformis DSM 13.
Bacteria; Firmicutes; Bacillales;
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Best Local
OBX4Vu
OBX4VU; O7ACUZ;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein Z3120 (Hypothetical protein EC
OrderedLocusNames=ECs2757, Z3120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-0157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE-21074935; PubMed-11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V. Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Buttin A., Shao V., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                         Q8X4V0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-2115231; PubMed-11280796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete gepome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
EMBL; AB005346; AAG56167.1; -.
EMBL; AB00537; BAB35624.1; -.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein 22097 (Hypothetical protein ECs2201).
OrderedLocusNames=ECs2201, z2097;
Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypotherical protein; Complete proteome.
SEQUENCE 103 AA; 11980 MW; 5A42AAF91CF29EB6 CRC64;
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STRAIN=0157:H7 / R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A90904; A90904.
C85713; C85713.
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6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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14; Mismatches
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Pred. No.
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5; Mismatches
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Pred. No. 71;
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Tobe T.,
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                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDIJINE=22423060; PubMed=12534463;

Nelson K.E., Weinel C., Paullen I.T., Dodson R.J., Hilbert H.,

Nelson K.E., Weinel C., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Martins dos Santos V.A.P., Pouts D.E., Jaugherty S.C., Kolonay J.F.,

Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,

Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

Modler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
"Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
EMBL; AE016779; AAN67137.1; -.
TIGR; PP1516; -.
GO; GO:0016020; C:membrane; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q88MQ4;
Q1-JUN-2003 (TrEMBLrel. 24,
Q1-JUN-2003 (TrEMBLrel. 24,
Q1-MAR-2004 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-0157:H7 / RIMD 0509952 / EHEC;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genomic comparison with a laboratory strain K-12.";
"Nama T., Ontonic comparison with a laboratory strain K-12.";
                                                                                                                                                                                       Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RND membrane fusion protein. OrderedLocusNames=PP1516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=160488;
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PIR; E90973; E90973.
Hypothetical protein
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MEDLINE=21074935; PubMed=11206551; DOJ=101.0138/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Res.
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STRAIN=0157:H7 / E
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Enterobacteriaceae; Escher
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Nature 409:529-533(2001).
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03 AA; 12092 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
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Pred. No. 30;
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D4F3CEA5A1089D30 CRC64;
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M., Tobe T.,
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RESULT
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 Query Match
Best Local S
Matches 7
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=A/duck/Hokkaido/9/99;
Liu J., Okazaki K., Kida H.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Removes the terminal sialic acid from carbohydrate chains of the host cell surface proteins and from the viral envelope. Such a reaction prevents self-aggregation and faci the mobility of the virus to and from the site of infection
                                                                                InterPro; IPR001860; Glyco hydro_34.
InterPro; IPR011040; Sialidase.
Pfam; PF00064; Neur; 1.
ProDom; PD000641; Glyco_hydro_34; 1.
Glycoprotein; Glycosidase; Hydrolase;
NON_TER 1
                                                                                                                                                            STRAIN-A/dudk/Hokkaido/9/99;
PubMed=14618990; DCI=10.1023/A:1026304117797;
Liu J.H., Okazaki K., Shi W.M., Kida H.;
"Phylogenetic analysis of hemagglutinin and neuraminidase
"Phylogenetic analysis of hemagglutinin and neuraminidase
"Phylogenetic analysis of hemagglutinin and neuraminidase
"Phylogenetic analysis of hemagglutinin and neuraminidase
"Phylogenetic analysis of hemagglutinin and neuraminidase
"Phylogenetic analysis of hemagglutinin and neuraminidase
"Phylogenetic analysis of hemagglutinin and neuraminidase
"Phylogenetic analysis of hemagglutinin and neuraminidase";
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Pfam; PF00529; HlyD; 1.
TIGRPAMs; TIGR01730; RND mfp; 1.
Complete proteome.
Complete 366 AA; 39409 MW; 9143D23CA7309658 CRC64;
                                                         NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Influenza A virus (A/duck/Hokkaido/9/99(H9N2)).
Viruses, ssRNA negative-strand viruses, Orthomy
Influenzavirus A; H9N2 subtype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 05-JUL-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6VS51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=249173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virus Genes 27:291-296(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuraminidase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                    similarity).

CATALYTIC ACTIVITY: Hydrolysis of alpha-(2->3)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->6)-, alpha-(2->8)-glycosidic linkages of terminal sialic residues in oligosaccharides, glycoproteins, glycolipids, colominic acid and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0008565; F:protein transporter activity; IEA. GO:0009306; P:protein secretion; IEA. erPro; IFA006143; HIYD. m; PF00529; HIYD; 1.
                                                                                                                                                                                                                                                                                                synthetic substrates.
SUBUNIT: Homotetramer
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 Similarity 29.7 Conservative
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                                                         43901 MW;
 51.3%; So
29.2%; Pi
tive 13;
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Last
Score 58; DB
Pred. No. 1.4e
13; Mismatches
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                                                         6D5C9DAA83DE658C CRC64;
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                                                                                                Transmembrane
                1.4e+02;
                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Orthomyxoviridae;
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                          Length 398;
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RESULT 15
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Q8XND2
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Best Local S
Matches 7
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Q8XND2;
01-MAR-2002
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01-NOV-1991
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21664373; PubMed=11792842; DOI=10.1073/pnas.022493799; Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
                       This
                                                                                                                                                                             Hofmann S.L., Topham M., Hsieh C.-L., Francke U "CDNA and genomic cloning of HRC, a human sarco protein, and localization of the gene to human chromosome 7.";
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clostridium perfringens.
Bacteria; Firmicutes; Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OrderedLocusNames=CPE0406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002
01-JUN-2003
                                                                                                                                                          Genomics 9:656-669(1991).
                                                                                                                                                                                                                                                            MEDLINE=91244309; PubMed=2037293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable reticuline oxidase.
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., FISSUE=Skeletal muscl
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           flesh-eater.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=HRC; Synonyms=HCP;
                                                                                                                                                                                                                                                                                                                                                                                                                              iomo gapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                            FUNCTION: May play a role in the re
sequestration or release in the SR
SUBCELLULAR LOCATION: Sarcoplasmic
SIMILARITY: Strong, to rabbit HRC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; AP003186; BAB80112.1; -.
GO:0006118; P:electron transport;
m; PF01565; FAD_binding_4; 1.
SWISS-PROT entry is copyright. It is produced through a deen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
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(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 20, Created)
(Rel. 20, Last sequence update)
(Rel. 44, Last annotation update)
reticulum histidine-rich calcium-binding
                                                                                                                                                                                                                                                                                                                                                                                                                              (Human)
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                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                  VARIANTS
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Last annotation update)
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Pred. No. 1.6e+0;
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                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70DF01B33B287EDD CRC64;
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                                                                                                           regulation of calcium SR of skeletal and car
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                                                                                                                                                                                                  Francke U.;
uman sarcoplasmic reticulum
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GO; GO:0005509; F:calcium ion binding; TAS.
GO; GO:0006936; P:muscle contraction; TAS.
Calcium-binding; Polymorphism; Repeat; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         VARIANT
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                                    699 AA;
                                                                                        50.9%; Score 57.5; DB 1; Length 699; liarity 36.0%; Pred. No. 3e+02; Conservative 11; Mismatches 4; Indels 1
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Glu-rich (acidic).
Asp-rich (acidic).
4 X tandem repeats, acidic.
1-1.
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S -> A (in dbSNP:3745297).

/FTId=VAR_005623.
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score greater than or and is derived by anal Pred. No. is the number of results predicted by chance to have a ater than or equal to the score of the result being printed, rived by analysis of the total score distribution.

# SUMMARIES

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The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I) which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microcitire plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it

New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding modules.

WPI; 2003-031166/03.

Claim 7; Page 16; 18pp; German.

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# ALIGNMENTS

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RESULT 3 ABP60370 ID ABP6

ABP60370 standard;

peptide;

36

B

28-MAR-2003 ABP60370;

(first entry)

binding peptide SEQ ID NO

protein chip; microtitre plate; detection

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WSHPQFEKXXXXXXXXXXXWSHPQFEK 27 WSHPQFEK---XXXXXXXXXWSHPQFEK 24

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Pred. No. 5.9e-06; 0; Mismatches 0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
                                                                                                                                                                                                                                 (BIOA-) INST BIOANALYTIK GMBH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Key Region

Location/Qualifiers 9. .28

"GGGS repeats

2-5 optionally absent,

residues

Synthetic Streptavidin; Streptavidin

Region

/label= GGGS\_repeat

DE10113776-A1.

The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain Streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, Ce.g. on protein chips or microtitre plates. The modules in (I) bind Strongly to streptavidin, with a co-operative effect that provides Stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention Sequence Disclosure; Page 4; 18pp; German New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding 24 AA,

Claim 8; Page 16; 18pp; German.

New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding

WPI; 2003-031166/03.

21-MAR-2001; 2001DE-01013776 21-MAR-2001; 2001DE-01013776

(BIOA-) INST

BIOANALYTIK GMBH GOETTINGEN.

87 . 28; Score 98.5; В <u>ი</u> Length

O'A

Query

Match

밁 S Matches Query Match The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Prox where x = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein as (PP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides erronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention Sequence 36 AA; 16; 1 WSHPQFEK-----XXXXXXXXXXXXXXSHPQFEK Similarity WSHPQFEKGGGSGGGSGGGSGGGSWSHPQFEK 36 Conservative 87.2%; St. 44.4%; Previous 11; Score 98.5; DE Pred. No. 1.1e-11; Mismatches DB 6; 27 0; Length Indels 36 9 Gaps 1:

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RESULT 5
ADS20251
ID ADS2
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AC ADS2
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                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-x where x = Gln, Asm or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein as (FP), also for detecting FP, e.g. on protein chips or microttre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying PP from dilute solution in batch formats (which uses simpler apparatus than column methods and result in lower loss of PP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
        ADS20251;
                                                          ADS20251 standard; protein; 646 AA
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 4; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated peptide, protein, comprises at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-031166/03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001DE-01013776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptavidin; protein chip; microtitre plate; detection.
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                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                              24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
9. .18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'label= unknown
                                                                                                                                                                                                                                                                                                                                         61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful as affinity purification tag for recombinant least two high-affinity streptavidin-binding
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                                                                                                                                                                                                                                                                                                                                           Score 69.5;
Pred. No. 0.
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RESULT 6 ADS20230 ID ADS2

ADS20230 standard; protein; 858

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Best Local S
Matches 10
                                                                                                                                                       disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAMTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAMTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The protein of the invention demonstrates osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of a human aggrecanase modified ADAMTS4 (mTS4) protein of the
                                                                                                                                                                                                                                                                                                                                                                                                    New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity fo treating aggrecanase-associated conditions, including osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unrombospondin type 1 motif 4; reprolysin; zinc metalloprotease; aggrecanase; osteopathic; antiinflammatory; antiarthritic; antir cytostatic; osteopathritis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's dis
                                                                                                                Sequence 646 AA;
                                                                                                                                                                                                                                                                                                                                              The invention
                                                                                                                                                                                                                                                                                                                                                                         Claim 9; SEQ ID NO 49; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-143860/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUL-2002; 2002US-0398721P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-FEB-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004011637-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; chromosome 1q21-q23; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; reprolysin; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human aggrecanase modified ADAMTS4 (mTS4) protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-2004 (first entry)
                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LAVA/)
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                                                        Local Similarity
nes 10; Conserv
615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RACIE L A.
MCDONAGH T.
FREEMAN B A.
GEORGIADIS K I
LAVALLIE E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORCORAN C FLANNERY C ZENG W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BA.
                  WSHPQFE-----KXXXXXXXXXXXXXWSHPQFEK 27
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WLHRRAQILEILRRRPWAGRKGSAWSHPQFEK 646
                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georgiadis
                                                                                                                                                                                                                                                                                                                                              relates to a novel isolated,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Flannery CR,
Jeorgiadis KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽.4
                                                                   59.7%;
31.2%;
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                                                         14;
                                                      Score 67.5; DI
Pred. No. 17;
14; Mismatches
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Lavallie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ER;
                                                                                    DB
                                                                                                                                                                                                                                                                                                                                              modified ADAMTS4
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                                                                                  Length
                                                         Indels
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                                                                                       646;
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                                                         Gaps
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18-NOV-2004 (first entry)

ADS20230,

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Best Matches

Local Similarity 31.2 hes 10; Conservative

Page 4

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The invention relates to a novel isolated, modified ADAMTS4 (a disintegrin-like and metalloprotease (reprolysin type) with the compared of a naturally occurring, full-length ADAMTS4 (a protein differs from the naturally-occurring, full-length ADAMTS4 protein, where the modified by at least one amino acid. ADAMTS proteins are a subfamily of zinc protein of the invention demonstrates oserate a subfamily of zinc for treating aggreganase-associated conditions, antirheuric and cytostatic and cytostatic antirhial members. The carrier, inflammatory joint disease, rheumatoid archivitis, periodontal disease and Crohn's disease. The current sequence is that of the human aggreganase ADAMTS4 truncated protein with insert
                                  Query Match
                                                                                                                                                                                                        New isolated, modified ADAMTS4 (aggrecanase) protein with improved treating aggrecanase-associated conditions, including osteoarthritis.
                                                                                                                                                                                                                                                                                    WPI; 2004-143860/14.
                                                                                                                                                                                                                                                                                                               Corcoran CJ, Freeman BA, C
                                                                                                                                                                                                                                                                                                                                                                      FREE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JUL-2002; 2002US-0398721P.
                                                                                                                                                                                                                                                                                                                                                                                                                            (AMHP ) WYETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        <sup>29</sup>-UUL-2003; 2003WO-US023484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004011637LA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
Synthetic.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADAWTS4; a disintegrin-like and metalloprotease; thrombospondin type I motif 4; reprolysin; zinc metalloprotease; eytostatic; osteopathic; antiinflammatory; antiarthritic; antiinflammatory; antiarthritic; antiinflammatory; antiarthritic; antiinflammatory; antiarthritic; antiinflamman; enzyme; chromosome 1921-923; truncation; Strep tag; mutant; enzyme; chromosome 1921-923; truncation; Strep tag; mutant;
                                                                                                                                                                                                                                                                                                                                   ZENG, W.
RACIB L A.
MCDONAGH T.
FREEMAN B A.
GEORGIADIS K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human aggrecanase ADAMTS4 truncated protein with
                                                                                                                                                                                                                                                                                                                                                                                                 CORCORAN C J.
                                                                                                                                                                                                                                                                                                   Flannery CR,
Georgiadis KE,
                      59.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Flexible spacer/enterokinase recognition site 848. 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Strep tag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
            Score 67.5;
                                                                                                                                                                                                                                                                                   Zeng W, Racie LA, Mcdonagh r_i
            DB
         ,
8
Length 858;
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The invention relates to human nucleic acids (AAIS7798-AAIS1369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, for imministypressant and cyrostatic acityity. The polypucleotides of the invention may be used to treat diseases of the polypucleotide of the invention may be used to treat diseases of the peripheral nervous injuries of the peripheral nervous acityities, peripheral nervous system diseases, buth as a partials and central nervous system diseases, such as a cartyinininhibin activity, chemotactic/chemotatheet also receptor activity, cancer disease, suppression, compared the peripheral nervous system disease, and strombolytic activity, chemotactic/chemotatheet assignment of the activity, cancer dispuses include the compared activity, cancer dispuses include the compared activity, cancer dispuses and therapy, drug screening, compared activity, arthritis and inflammation, leukaemias and the printed specification.
                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999;
21-JAN-2000; 2000US-00481275.
25-ARR-2000; 2000US-00582317.
20-UUN-2000; 2000US-00582317.
19-UUL-2000; 2000US-0058042.
10-AUG-2000; 2000US-00620312.
14-SEP-2000; 2000US-006823151.
19-OCT-2000; 2000US-00682191.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                 Example 2; SEQ ID NO 5690; 10078pp; English.
                                                                                                                                                                                                                     Novel nucleic acids and polypeptides, useful for treating disorders such
                                                                                                                                                                                                                                                                                                  WPI; 2001-442253/47.
N-PSDB; AAI59915.
                                                                                                                                                                                                                                                                                                                                             Tang YT,
Wang J,
Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; Altheimer: s; Parkinson; alterapy; central nervous system; neuropathy; central nervous system; cheuropathy; central nervous system; cus; chemokinetic; thrombolytic; drug screening; syndrome; chemotactic; neuropathy; chemotactic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polypeptide SEQ ID NO 5690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM40759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM40759 standard; protein; 490 AA
                                                                                                                                                                                                                                                                                                                              Wang Z, Wehrman T, Goodrich R, Drmanac
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hrman T, Xu C, )
Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                 Ma Y,
Xue AJ,
                                                                                                                                                                                                                                                                                                                       Qian XB,
, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
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Zhang J,
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J, Zhao QA;
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The invention relates to a novel isolated, modified ADAMTS4 (a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAMTS4 protein, where the modified protein differs from the naturally-cocurring, full-length ADAMTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The
                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                             New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity for treating aggrecanase-associated conditions, including osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORC/)
(FLAN/)
(ZENG/)
(RACI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-FEB-2004
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Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type I motif 4; reprolysin; zinc metalloprotease; thrombospondin type I motif 4; reprolysin; zinc metalloprotease; antirheuma aggrecanase; osteopathic; antiinflammatory; antiarthritic; antirheuma cytostatic; osteopathitis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's disease; human; chromosome 1q21-q23; enzyme; truncation; mature; furin cleavag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Furin-processed human
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FREEMAN B A.
GEORGIADIS K I
LAVALLIE E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RACIE
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                                                                                                                                                                                                      SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Flannery
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                                                                                                                                                                                                      47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
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wild-type replaced by Strep tag"
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                                                                                                                                                                                                117pp; English
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Pred. No. 13;
L3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    Zeng W, Raci
Lavallie ER;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Racie LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mcdonagh
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                       ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; reprolysin; zinc metalloprotease aggrecamase; osteopathic; antiinflammatory; antiarthritic; anticytostatic; osteopathitis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's dihuman; enzyme; chromosome 1q21-q23; truncation; Strep tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention demonstrates osteopathic, antiinflammatory, antiarhritic, antirheumatic and cytostatic activities and may be useful for treating aggrecannase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of the furin-processed human aggrecanase ADAMTS4 truncated protein with Strep tag of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                       New isolated, modified ADAMTS4 (aggrecanase) protein with improved stability useful for identifying inhibitors of the enzyme activity treating aggrecanase-associated conditions, including osteoarthriti
                                                                                                                                                                                                          (AMHP)
(CORC/)
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Unidentified.
                                                                                    WPI; 2004-143860/14.
                                                                                                           Freeman
                                                                                                                      Corcoran
                                                                                                                                                                           (MCDO/)
                                                                                                                                                                                                                                                        29-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                          Misc-difference
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                                                                                                                                                                                                  (ZENG/)
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FLANNERY C
ZENG W.
                                                                                                                                           FREEMAN B A.
GEORGIADIS K I
LAVALLIE E R.
                                                                                                                                                                           RACIE L A. MCDONAGH T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 697
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                                                                                                        Flannery C
Georgiadis
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                                                                                                          Zeng W, R
Lavallie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 66; UB (
Pred. No. 18;
13; Mismatches
                                                                                                           Racie
e ER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strep
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                                          osteoarthritis.
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                                                      for
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                                                                                                                                                                                                                                                                                                                                                tag"
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The invention relates to a novel isolated,

modified

ADAMTS4

9;

SEQ

ID NO 24; 117pp; English.

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ARESULT 10
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choline-binding protein; CbpG; vaccine; immune response; antibacterial; CbpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-2003
22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE24889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE24889 standard;
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                                                                                                                                                                                                                                                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pneumococcus, sp. choline-binding protein, CbpA #4.
                                                                                                      Misc-difference
                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        697 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                     /label= Unknown
/note= "Encoded by TGA of the inverse complementary
strand of the sequence shown in Fig 1 (AAD40149)"
108
                                                                                                                                 /label= Unknown
/note= "Encoded by TGA of the inverse
strand of the sequence shown in Fig 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Unknown
/note= "Encoded by TGA of the inverse
strand of the sequence shown in Fig 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strand of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                       /label= Unknown
/note= "Encoded by TGA of the inverse complementary
                                                                                                                                                                                                                                                 /label= Unknown
/note= "Encoded by TGA of the inverse
strand of the sequence shown in Fig 1
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/note= "Encoded by TGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Encoded by TGA of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB
Pred. No. 31;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the inverse
shown in Fig 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the inverse
shown in Fig 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementary (AAD40149)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complementary (AAD40149)"
                                                                                                                                 complementary (AAD40149)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complementary (AAD40149)"
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                                                                                                                                                                                                                                                    complementary (AAD40149)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.
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                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to choline-binding protein (CbpG) and its corresponding nucleic acid. Vaccines that contain CbpG, its N-truncated version or nucleic acid encoding them are useful for preventing infection by bacteria that express CbpG, specifically Streptococcus pneumoniae and in inducing an immune response. Compositions that contain CbpG or antibodies specific for it are useful for treating such infections. Antibodies are also useful for diagnostic detection of CbpG and oligonucleotides that hybridise to CbpG DNA are used to detect CbpG-expressing bacteria. CbpG DNA are used for recombinant production of CbpG and their fragments. The present sequence is Pneumococcus sp. CbpA protein. (Updated on 06-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated streptococcal choline-binding protein CbpG, useful for treatment of streptococcal infections and in protective vaccines, also related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                             Sequence 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US2002041881-A1
                                                                                      Bilin-binding
                                                                                                              Bilin binding-protein associated protein #6.
                                                                                                                                                                                          AAB46425 standard; protein; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAD40149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tuomanen EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TUOM/) TUOMANEN E I.
(GOSI/) GOSINK K.
(MASU/) MASURE R.
                                     WO200075308-A1
                                                              Unidentified
                                                                                                                                         06-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-488715/52.
                                                                                                                                                                                                                                                           75
                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                         WSHPVAIEPLAFRXYHEPLYWSHP
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                         (first entry)
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                                                                                      protein;
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/note= "Encoded by TGA of the
strand of the sequence shown
179
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                                                                                                                                                                                                                                                                                                             56.2%; Score 63.5; D
41.7%; Pred. No. 9.4;
vative 10; Mismatches
                                                                                         mutein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Masure
                                                                                       BBP; digoxigenin.
                                                                                                                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the inverse complementary strand in Fig 1 (AAD40149)"
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in Fig 1
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                                                                                                                                                                                                                                                                                                                                     Length 179;
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08-JUN-2000; 2000WO-DE001873

99DE-01026068

(SKER/)

SKERRA

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RESULT 12
ADO19051
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Best Local S
Matches 10
                                                                                                                                                                                                                                         Mouse; antibody; M1 Fab; heavy chain; Fab; scFv; abused drug; morphine; THC; amphetamine; environmental hazard; toxic compound; microbial process; metabolic process; drug monitoring;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel polypeptides (I) that are muteins of bilin binding protein (BBP), which can bind digoxigenin (Dig) or its conjugates, do not bind ouabain, testosterone or 4-aminofluorescein, and have an amino acid (aa) substitution at at least one of the positions 28, 31, 34-37, 58, 60, 69, 88. 90, 95. 97, 114, 116, 125 or 127. (I), or its fusion proteins, are used to bind, detect, determine, immobilize or separate Dig or its conjugates with proteins, nucleic acids, carbohydrates, other biological or synthetic macromolecules or low molecular weight compounds, particularly in assays where Dig is being used as a label. Compared with Dig-specific antibodies, (I) have a simpler structure and are easier to prepare. They have very high specificity for Dig, relative to other steroids, and fusion partners may be attached to either end without compromising their ability to bind
                                                                                                                                                                                                                                                                                                    Murine antibody M1 Fab fragment heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                         ADO19051 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
WPI; 2004-420710/39
                                                                                                                                          03-JUN-2004
                                                                                                                                                                                                                             pharmacological research.
                                                                                                                                                                                                                                                                                                                                  26-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New muteins of bilin-binding protein, useful for detecting digoxigenin being used as label in e.g. binding assays, are very selective for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skerra A,
                         Pulli T,
                                                                                                            17-NOV-2003; 2003WO-FI000875
                                                                                                                                                                       WO2004046733-A1
                                                                                 18-NOV-2002; 2002FI-00002048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-071071/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WSHPQFEKXXXXXXXXXXXX 20
                                                      VALTION TEKNILLINEN TUTKIMUSKESKUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WSHPQFEKKXASGRFMKKGF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 448 AA;
                         Hoeyhtyae M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlehuber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%;
                                                                                                                                                                                                                                                                                                                                                                                         protein; 236
                         Takkinen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 63; DB pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                           Soederlund
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 448;
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RESULT 13
AD019053
ID D019053
AD019053
AC AD019
XX AD019
XX Murin
XX Muse
KW THC,
KW micrc
KW micrc
KW micrc
KW micrc
KW micrc
KW micrc
KW Darn
XX Darn
OS Mus E
XX O3-JI
XX IB-N
XX VALI
PF 17-N
XX WPI,
PT NOn-I
PT Non-I
PT reag
PT parti
XX Clai
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          analyte, comprising reacting a sample containing the analyte with a reagent pair comprising a first binding partner that binds to the analyte and a second binding partner that binds to the complex of the analyte and the first binding partner, and determining the binding of the second binding partner, and determining the binding of the second binding partner, thus indicating the presence of the analyte in the sample. The first and second binding partners are antibody fragments for a small analyte, particularly for assaying drugs of abuse e.g., morphine, THC or amphetamine. The immunoassay is useful for detecting environmental hazards, toxic compounds in food and feed, chemicals indicative of processes (e.g., microbial processes in buildings, metabolic processes of living organisms) and in clinical tests, drug monitoring and pharmacological research. This sequence represents the murine antibody M1 Fab fragment heavy chain, used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-competitive immunoassay for small analyte, useful for assaying drug of abuse (e.g., morphine), comprises reacting a sample of analyte with reagent pair comprising a first binding partner and a second binding
                                                                                                                                                                                                                                                                                                                                                                                      Mouse; antibody; M2 Fab; heavy chain; Fab; scFv; abused THC; amphetamine; environmental hazard; toxic compound; microbial process; drug monitoring; pharmacological research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 21; SEQ ID NO 2; 35pp; English
                                                                                                                                                                                                                                                                                                                         WO2004046733-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADO19053 standard;
                                                                                                                                                            Pulli T,
                                                                                                                                                                                                                                                           17-NOV-2003; 2003WO-FI000875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine antibody M2 Fab fragment heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
                                                                                                                            WPI; 2004-420710/39
                                                                                                                                                                                           (VALW )
                                                                                                                                                                                                                           18-NOV-2002; 2002FI-00002048
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                                                                                                                                                                                            VALTION TEKNILLINEN TUTKIMUSKESKUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPASSTKVDKKIVPRDCGTSWSHPQFEK 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 236
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                                                                                                                                                            Σ,
                                                                                                                                                            Takkinen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a non-competitive immunoassay for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
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Pred.
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                                                                                                                                                            Soederlund
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                                                                                                                                                                                                                                                                                                                                                                                                                                        drug; morphine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ų.
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Non-competitive immunoassay for small analyte, useful for assaying d of abuse (e.g., morphine), comprises reacting a sample of analyte wi reagent pair comprising a first binding partner and a second binding

Claim partner.

21;

SEQ

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35pp; English

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a non-competitive immunoassay for a small canalyte, comprising reacting a sample containing the analyte with a creagent pair comprising a first binding partner that binds to the analyte can a second binding partner that binds to the complex of the analyte and the first binding partner, and determining the binding of the second binding partner, and determining the binding of the second conding partner, thus indicating the presence of the analyte in the cample. The first and second binding partners are antibody fragments Fab cor serv. The reagent pair is useful in a non-competitive immunoassay for a small analyte, particularly for assaying drugs of abuse e.g., morphine, cor amphetamine. The immunoassay is useful for detecting environmental congoing processes (e.g., microbial processes in buildings, metabolic congoing processes (e.g., microbial processes in buildings, metabolic processes of living organisms) and in clinical tests, drug monitoring and pharmacological research. This sequence represents the murine antibody M2 corrections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 10
                                                                                                                                                                              Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                          12-OCT-2000; 2000US-0240465P.
                                                                                                                                                                                                                                                                                                                                                                                                       18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200230962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic cadmium/mercury ion binding chelon protein
                                                                                                                                                                                                                                                                                                               (UYGE-)
                                                                                                                                                                                                                                                                                                                                                                       12-OCT-2001; 2001WO-US031819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 AA;
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                                                                                                                                                                                                                                                                                 Caguiat JJ;
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1:

The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The

The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host

capable

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expressing

coding

with a vector

Claim

22; 42pp; English.

Claim

4.

Page

English.

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ARESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC nucleic acid encoding the chelon protein is useful for binding divalent CC mercuric ions, to take up, sequester and concentrate the heavy metal ions CC from contaminated soil, ground water, hydroponic solutions or irrigation CC water of waste streams. The DNA of the invention, when immobilised onto a CC solid support, is useful for concentrating heavy metal ions from CC contaminated environment waste streams or contaminated aqueous medium CC including biological fluids. The nucleic acid, when recombinantly CC expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), CC is suitable for use in the in vivo sequestration and elimination of CC mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of CC the invention is highly specific and binds divalent cation such as CC mercury or cadmium with high affinity. The present amino acid sequence condition mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons of the invention.
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                                                                                                                                                                                                                Novel non-naturally occurring recombinant DNA molecule encoding a cheprotein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids.
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8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEORGIA RES FOUND INC
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Mismatches
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CC comprising a promoter active in the host cell operably linked to a coding CC region for the protein to produce a recombinant host cell and culturing CC the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent CC mercuric ions, to take up, sequester and concentrate the heavy metal ions CC from contaminated soil, ground water, hydroponic solutions or irrigation CC water of waste streams. The DNA of the invention, when immobilised onto a CC solid support, is useful for concentrating heavy metal ions from CC contaminated environment waste streams or contaminated aqueous medium CC including biological fluids. The nucleic acid, when recombinantly CC expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of CC mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as CC mercury or cadmium with high affinity. The present amino acid sequence cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons of the convention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
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ঠ Search completed: March Job time : 121.61 secs 밁 Query Match 54.9%; Score 62; DB Best Local Simflarity 42.1%; Pred. No. 8.2 Matches 8; Conservative 11; Mismatches

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8 15 US-10-424-599-184769

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#### ALIGNMENTS

RESULT 1 US-10-026-578B-3

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Sequence 3, Application US/10026578B
Publication No. US20030083474A1
GENERAL INFORMATION:
APPLICANT: IBA (GmbH)
APPLICANT: ISA (GmbH)
APPLICANT: Schmidt, Thomas
ITILE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100610.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 24
TYPE: PRT
ORGANISM: Artificial sequence
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FEATURE:
NAME/KEY: MISC_FEATURE
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LOCATION: (9)...(9)
OTHER INFORMATION: X represents a single amino acid
LOCATION: (11) ... (11)
OTHER INFORMATION: X represents a single amino
                                                                                                                                                                                                                                                                                                                      NAME/KEY: MISC_FEATURE
LOCATION: (10)..(10)
OTHER_INFORMATION: X represents
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OTHER INFORMATION: Synthetic Peptide
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                                                                                    Query Match
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Best Local :
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CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: IBA (GmbH)
APPLICANT: Schmidt,
                                                                                                                     NAME/KEY: misc feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
                                                                                                                                                                            OTHER INFORMATION: X represents a single amino acid at each of the positions indicat OTHER INFORMATION: ed; some of the amino acids may be missing. Where amino acids are OTHER INFORMATION: missing, the total numbers of x will be no less than 5
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                OTHER INFORMATION: Synthetic Peptide
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OTHER INFORMATION: Artificial Sequence
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LOCATION: (14)...(14)
OTHER INFORMATION: X represents a single amino
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                                                                      Local Similarity
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     1 WSHPQFEK-----
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88.9%;
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Pred. No. 6.8e
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US-10-026-578B-11
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GENERAL INFORMATION:
                      Query Match
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Publication No. US2
GENERAL INFORMATION
                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: EP 00103551.8 PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT EILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733Alel methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/026,578B CURRENT FILING DATE: 2002-11-11 PRIOR APPLICATION NUMBER: DE 101 13 776.1 PRIOR FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: PCT/EP01/11846 PRIOR FILING DATE: 2001-10-12
                                                                                                          TYPE: PRT
ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity FILE REFERENCE: 100810.01US1
                                                                    OTHER INFORMATION: Description of Artificial Sequence: synthetic
                                                                                                FEATURE:
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APPLICANT: Sch
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No. US20030083474A1
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45.8%;
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Score 69.5; DB Pred. No. 0.22;
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Pred. No. 0
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US-10-026-578B-4
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LENGTH: 24
TYPE: PRT
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity '
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: DETT/EP01/11846
PRIOR APPLICATION NUMBER: DETT/EP01/11846
PRIOR APPLICATION STEP : 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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FEATURE:
OTHER INFORMATION: Synthetic Peptide
FEATURE:
NAME/KEY: MISC FEATURE
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FEATURE
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APPLICANT: Schmidt,
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OTHER INFORMATION: X represents
                                                                                                           NAME/KEY: MISC_FEATURE
LOCATION: (17)..(17)
OTHER_INFORMATION: X represents
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OTHER INFORMATION: X represents
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                                                               NAME/KEY: MISC_FEATURE LOCATION: (18)..(18)
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OTHER INFORMATION: X represents a
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OTHER INFORMATION: X represents
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NAME/KEY: MISC_FEATURE LOCATION: (22)..(22)
                                                OTHER INFORMATION: X represents
                                                                                                                                                                                           NAME/KEY: MISC FEATURE LOCATION: (16)..(16)
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          Sequence 1, Application US/10887228A

Publication No. US20050037402A1

GENERAL INFORMATION:

APPLICANT: Schering AG

TITLE OF INVENTION: Device and Process for Direct Quantitative in v
TITLE OF INVENTION: Substance That is Contained in a Sample
FILE REFERENCE: S30569US

CURRENT APPLICATION NUMBER: US/10/887,228A

CURRENT APPLICATION NUMBER: D103 31 093.2

PRIOR APPLICATION NUMBER: D3 103.2

PRIOR FILING DATE: 2003-07-09

PRIOR FILING DATE: 2003-07-16

NUMBER DF SCT TANCE 12005-07-16

NUMBER DF SCT TANCE 12005-07-16
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US-10-887-228A-1
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Best Local
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   SEQ ID NOS:
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Sequence 34, Application US/09809517A

Patent No. US2002034733A1

GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1e1 methods for dis
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11

CURRENT APPLICATION UNMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
; OTHER INFORMATION: Artificial Sequence represents
US-10-026-578B-4
                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
SEQ ID NO 34
LENCTH: 25
TYPE: PRT
                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 41
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NAME/KEY: MISC FEATURE
TOTATION: (24)...(24)
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NAME/KEY: MISC_FEATURE
LOCATION: (23)..(23)
OTHER INFORMATION: X represents
                                                                                                                                                             ORGANISM: artificial sequence FEATURE:
                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: synthetic module
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OTHER INFORMATION: X represents
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                              5 QFE-KXXXXXXXXXXXXXXXBHPQFEK 27
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FEQKLISEEDLNGAPWSHPQFEK
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                                                                Conservative
                                                                            61.5%;
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                                                                               Score 69.5; DB Pred. No. 0.23;
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Pred. No. 0.
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APPLICANT: Schering AG
ITITLE OF INVENTION: Device and Process for Di.
ITITLE OF INVENTION: Substance That is Contai:
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ITILE OF INVENTION: UNMBER: US/10/887,228A
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: DE 103 31 093.2
PRIOR APPLICATION NUMBER: US 60/478,262
PRIOR APPLICATION NUMBER: US 60/478,262
PRIOR FILING DATE: 2003-07-16
INUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 246
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; OTHER INFORMATION: Fab fragment of variable heavy chain
US-10-887-228A-9
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US-10-887-228A-1
                                                                                                                                                                                                                       Sequence 5, Application US/10887228A
Publication No. US20050037402A1
GENERAL INFORMATION:
APPLICANT: Schering AG
TITLE OF INVENTION: Device and Process for Direct Quantitative in vitro
TITLE OF INVENTION: Substance That is Contained in a Sample
FILE REFERENCE: S30569US
                                  SOFTWARE: PatentIn version 3.1 SEQ ID NO 5
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                                                                             CURRENT APPLICATION NUMBER: US/10/887,228A CURRENT FILING DATE: 2004-07-09 PRIOR APPLICATION NUMBER: DE 103 31 093.2 PRIOR FILING DATE: 2003-07-09 PRIOR APPLICATION NUMBER: US 60/478,262 PRIOR APPLICATION NUMBER: US 60/478,262 PRIOR FILING DATE: 2003-07-16 NUMBER OF SEQ ID NOS: 12
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LENGTH: 252
TYPE: PRT
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EFEQKLISEEDLNGAPWSHPQFEK 246
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45.8%; Pred. No. 4.4,
tive 12; Mismatches
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Pred. No. 4.4;
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_137862C.1.pep
US-10-424-599-184769
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US-10-424-599-184769
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; OTHER INFORMATION: Fab fragment of variable heavy chain
US-10-887-228A-5
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                                                                                CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 184769
LENGTH: 158
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                                                                                                                                                                                                                                                                                         Sequence 184769, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
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SEQ ID NO 104065
LENGTH: 134
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Best Local Similarity 45...
11; Conservative
                                                                                                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
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                                TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_101434C.1.pep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 37.5
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Barbazuk, Brad
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. US20040123343A1
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Pred. No. 4.5;
12; Mismatches
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Pred. No. 3
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Score 68;

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Best Local S
Matches 9
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SEQ ID NO 200150
LENGTH: 252
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SEQ ID NO 184075
                                                        Matches
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Best Local
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                   APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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APPLICANT: Kovalic David K
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                                                                                                                                                            ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                          OTHER INFORMATION: Clone ID: PAT_MRT4530_95648C.1.pep
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Conservative
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13; Mismatches
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RESULT 15
US-10-628-432-27
IS-quence 27, Application US/10628432
Publication No. US20040142863A1
GENERAL INFORMATION:
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; Sequence 49, Application US/10628432
; Publication US20040142863A1
Search completed: March Job time: 84.9634 secs
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SEQ ID NO 27
LENGTH: 858
TYPE: PRT
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SEQ ID NO 49
LENGTH: 646
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Best Local Similarity
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CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
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CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
FILE REFERENCE: AM101378
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TITLE OF INVENTION: Modified ADAMTS4 molecules
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OTHER INFORMATION: furin-processed construct
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
Query
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                                                                                                                                                                                   Issued_Patents_AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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RESULT 1

US-09-809-517A-31

4 US-09-809-517A-31 4 US-09-809-517A-34 4 US-09-809-517A-30 4 US-09-809-517A-3 4 US-09-977-137A-4 4 US-09-977-137A-7 4 US-09-977-137A-8 4 US-09-977-137A-8 4 US-09-977-137A-8
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53 46.9 400 3 US-09-352-574-25-2 53 46.9 400 3 US-09-352-574-2 53 46.9 638 4 US-09-252-991A-25205 46.9 979 1 US-09-058-263-6 53 46.9 979 2 US-09-058-263-6 53 46.9 979 2 US-09-059-059-6 53 46.9 979 3 US-09-059-059-6 53 46.9 979 4 US-09-455-962-6 53 46.9 979 5 PCT-US95-06530-6 53 46.9 979 5 PCT-US95-06530-6 53 46.9 979 5 US-08-811-949-65 54 46.0 27 2 US-08-310-912A-47 52 46.0 27 3 US-08-841-089-47 52 46.0 27 3 US-09-301-085-47 52 46.0 27 5 PCT-US95-04570-47 52 46.0 27 5 PCT-US95-0459-47 52 46.0 27 5 PCT-US95-04590-47 52 46.0 27 5 PCT-US95-04590-47 52 46.0 27 5 PCT-US95-04590-47 52 46.0 27 5 PCT-US95-04590-47 52 46.0 250 4 US-09-270-767-33709 52 46.0 250 4 US-09-270-767-33709 52 46.0 659 4 US-09-252-991A-26013	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
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US-08-621-255-2 US-09-352-991A-25205 US-09-252-991A-25205 US-09-252-991A-25205 US-09-252-66 US-09-058-264-6 US-09-058-264-6 US-09-058-264-6 US-09-058-264-6 US-08-811-949-65 US-08-811-949-65 US-08-811-949-65 US-08-811-949-67 US-08-310-912A-47 US-08-310-912A-47 US-08-310-912A-47 US-08-310-912A-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47 US-09-301-085-47	4.	4	4.	u	ഗ	w	w	N	N	ഗ	4	w	N	N	_	4.	w	L.
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	26013, A	33709, A	48926, A	47, Appl	47, Appl	47, Appl	47, Appl	47, Appl	65, Appl	6, Appli	6, Appli	6, Appli	6, Appli	•	<ol><li>Appli</li></ol>	25205, A	<ol><li>Appli</li></ol>	Z, Appli

#### ALIGNMENTS

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Sequence 31. Application US/09809517A

Patent No. 6753136

GENERAL INFORMATION:
APPLICANT: Lobning, Corinna
ITILE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on to the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (poly)peptides/proteins on the state of invention: No. 6753136el methods for displaying (po
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US-09-809-517A-34
; Sequence 34, Application US/09809517A
; Patent No. 6753136
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on b
TITLE OF INVENTION: particles via disulfide bonds
TITLE OF INVENTION: UNMBER: US/09/809,517A
CURRENT EPPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y Match 61.5%; Score 69.5; DB 4; Length 24; Local Similarity 45.8%; Pred. No. 0.0088;
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Best Local Similarity
Matches 9; Conserve
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                  SOFTWARE: PatentIn version 3.0
SEQ ID NO 33
LENGTH: 22
TYPE: PRT
                                                                   PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTY-
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TITLE OF INVENTION: No. 6753136el methods for displaying
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
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PRIOR APPLICATION NUMBER: EP 00103551.8
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CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
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TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
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SEQ ID NO 34
LENGTH: 25
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NUMBER OF SEQ ID NOS: 41
ORGANISM: artificial sequence
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EFEQKLISEEDLNGAPWSHPQFEK 25
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Pred. No. 0
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-33
                Query Match
Best Local S
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                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09977137A Patent No. 6750042 GENERAL INFORMATION:
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
TITLE OF INVENTION: Methods
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APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
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                                                                              INFORMATION: Description
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   Similarity 42.1
8; Conservative
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54.9%; Score 62; DB
42.1%; Pred. No. 1.2,
tive 11; Mismatches
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Pred. No. 0.04
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                                                                            of Artificial Sequence:
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US-09-977-137A-7
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                                                             Query Match
Best Local S
Matches 8
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 117
TYPE: PRT
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Patent No.
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APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonati
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
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                                                              Conservative
                                                         54.9%; Sco.
42.1%; Pre
Ative 11;
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                                                                              Score 62;
Pred. No.
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Pred. No.
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RESULT 9

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RESULT 11
US-09-977-137A-11
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US-09-977-137A-10
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Sequence 11, Application US/09977137A
Patent No. 6750042
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 117
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APPLICANT: Summers, Anne O
APPLICANT: Caguiat, Jonat
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Best Local
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Patent No. 6750042
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Best Local Similarity
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Patent No. 6750042
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Methods
TITLE OF INVENTION: Methods
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Pred. No.
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Query Match
Best Local Similarity
Watches 8; Conserve
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US-09-977-137A-12
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; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-977-137A-11
                                                                                                                                                                               Sequence 6, Application US/09977137A Patent No. 6750042 GENERAL INFORMATION:
   APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
TITLE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatehtIn Ver. SEQ ID NO 12
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 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
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ORGANISM: Artificial Sequence
FEATURE:
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2000-10-12
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42.1%; Pred. No. 1.2;
tive 11; Mismatches 0; Indels
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Pred. No. 1
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,180
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25931
LENGTH: 434
TYPE: PRI
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                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                    Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25931, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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SEQ ID NO 6
LENGTH: 118
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                                                                                                                    TITLE OF INVENTION: Special Constructs a TITLE OF INVENTION: Cyclin E NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pharmacia & Upjohn Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                   COUNTRY: U
                                                                                                CITY: Kalamazoo
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WSYPAFERAMRHGVARDGSYLYPAF
                                                                                                                                                                                                    Sharma, Satish K. Rank, Kenneth B. Evans, David B.
                                                                USA
                                                                                                             301 Henrietta Street
                                                                                                                                                                                                                                                     (Pharmacia & Upjohn, Co. alternatively, for U.S. Hollingsworth, Robert A.
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Pred. No.
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Page 5
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOPTWARE: Patentin Rel. #1.0, Ver. #1.25/WordPerfect 5.2+
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/895,707
FILING DATE: US/08/895,707
FILING DATE: US/08/895,707
FILING DATE: US/08/895,707
FILING DATE: US/08/895,707
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FILING DATE: US/08/895,707
FILING DATE: US/08/895,707

FILING DATE: US/08/895,707

RESISTRATION UNMBER: 35,004
REFERENCE/DOCKET NUMBER: 6054
TELEPHONE: 616-833-897
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
ELEPHONE: 616-833-897
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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SEQUENCE TYPE: Mainle acids
TYPE: Mainle acids
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TYPE: MAIN ACIds
STEANNEONESS: NO- 14:
FRAGMENT TYPE: N-terminal
US-08-895-707-7
ONETY MATCH
DATE: SOOTE 60; DB 3; Length 386;
MATI-SENSE: NO-
OPERATION: MAINLE SOOTE 60; DB 3; Length 386;
MATI-SENSE: NO-
OPERATION: MAINLE SOOTE 60; DB 3; Length 386;
MATI-SENSE: NO-
OPERATION: MAINLE SOOTE 60; DB 3; Length 386;
MATCHES 8; Conservative 11; Mismatches 3; Indels 0; Gaps
OPERATION: MAINLE SOOTE 60; DB 3; Length 386;
MATCHES 8; Conservative 11; Mismatches 3; Indels 0; Gaps
OPERATION: MAINLE SOOTE 60; DB 3; Length 386;
MATCHES 8; Conservative 11; Mismatches 3; Indels 0; Gaps
OPERATION: MAINLE SOOTE 60; DB 3; Length 386;
MATCHES 8; CONSERVANCENTERION 14;

DATE: MAINLE SOOTE 60; DB 3; Length 386;
MATCHES 8; CONSERVANCENTERION 14;

MATCHES 8; CONSERVANCENTERION 14;

MATCHES 9; CONSERVANCENTERION 14;

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MATCHES 9; CONSERVANCENTERION 14;

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Minimum DB
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46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.9	46.9	46.9	47.4	47.4	47.4	47.4		47.4
297	290	282	246	230	228	139	1091	553	211	801	685	617	537	507	484
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transport versicle	nuclear receptor N	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	conserved hypothet	contactin precurso	hybrid cluster [4F	hypothetical prot	glucosidase BH0704	c-di-GMP phosphodi	hypothetical prote	tyrosinase-related	hypothetical prote	glutamate-tRNA lig

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A44308
Antho-RPamide precursor - sea anemone (Anthopleura elegantissima)
C;Species: Anthopleura elegantissima
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44308
R;Schmutzler, C.; Darmer, D.; Diekhoff, D.; Grimmelikhuijzen, C.J.
J. Biol. Chem. 267, 22534-22541, 1992
A;Title: Identification of a novel type of processing sites in the precursor for the sea A;Reference number: A44308; MUID:93054550; PMID:1429603
A;Accession: A44308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
T25450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-435 < SCHy
A;Cross-references: UNIPROT:P10419; GB:M98269; NID:g155702; PIDN:AAA27738.1; PID:g155703
A;Note: sequence extracted from NCBI backbone (NCBIN:117102, NCBIP:117104)
C;Keywords: neuropeptide
                                                                                                                         A;Gene: CBSP:B0412.3
A;Map position: 3
A;Introns: 39/2; 70/1; 133/2; 288/3; 386/1; 470/3; 568/3; 631/2; 733/2; 819/3; 931/1; 96
C;Superfamily: Caenorhabditis elegans hypothetical protein B0412.3
                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1107 <BEN>
A;Cross-references: UNIPROT:P90984; EMBL:U80953; PIDN:AAB52556.1; GSPDB:GN00021; CESP:B0
A;Experimental source: strain Bristol N2; clone B0412
A;Experimental source: strain Bristol N2; clone B0412
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Bentley, D.

submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid B0412.
A;Reference number: Z20037
A;Accession: T25450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein B0412.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004 C;Accession: T25450
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Best Local Similarity
Matches 10; Conserv
Query Match 52.6%; Score 60; DB 2; Best Local Similarity 21.4%; Pred. No. 60; Matches 6; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 FSDPQFWKGRFSDPQFWKGRFSDPQFWK 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.6%; Score 60; DB ilarity 35.7%; Pred. No. 20; Conservative 14; Mismatches
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                                                                Length 1107;
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RESULT 5
T34497
                                                                                                                                                                                                                                                                                                                    C;Accession: T34497
R;Latreille, P.
                                                          hypothetical protein ZK1248.15 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex
submitted to the EMBL Data Library, June 1995 A; Description: The sequence of C. elegans cos
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C;Superfamily: glutathione S-transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: T40926
R;Volckaert, G; Wood, V; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, January 1999
A;Reference number: Z21957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein SPCC1281.07c - fission yeast (Schizosaccharoc;Species: Schizosaccharomyces pombe C:Date: 0.3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: T40926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note:
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A; Introns: 39/1; 74/3; 106/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:074345; EMBL;AL031536; NID:e1319499; PID:e1319504
A;Experimental source: strain 972h(-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transcription factor - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
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Best Local S
Matches 7
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ilarity 28.0%;
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Pred. No.
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Pred. No. 39
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                                                        29-Oct-1999 #text_change 09-Jul-2004
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26;
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hypothetical protein - Synechocystis sp.
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 2:
C;Accession: S76147
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 38/3 C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: T32G6.12; At2g41600
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:02222; EMBL:AC002510; NID:g2618683; PID:g2618695
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein At2g41600 [imported] - Arabidopsis thaliana k;Alternate names hypothetical protein T3266.12 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004 C;Accession: T00816; G84843 R;Rounsley, S.D. Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, November 1997 A;Description: Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence. A;Reference number: Z14163 A;Accession: T00816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-151 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A; Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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A;Molecule type: DNA
A;Residues: 1-151 <ROU>
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C;Superfamily: Caenorhabditis elegans hypothetical protein ZK1248.15; WW repeat homology
F;198-236/Domain: WW repeat homology <WWR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Experimental source: C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-652 <LAT>
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                  #sequence_revision 25-Apr-1997 #text_change
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25.0%; Pred. No.
tive 15; Mismatc
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C;Accession: E90973
R;Hayashi, T.; Makino, K.; Obgasawara, N.; Yasunaga, T.; F
DNA Res. 8, 11-22, 2001
A;Title: Complete genome seq.
A;Reference number: A99629; N
A;Accession: E90973
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C;Superfamily
C;Keywords: t
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C 4.2.3.9 aristolochene synthase () - Penicillium roqueforti
C;Species: Penicillium roqueforti
C;Date: 21-Sep-1993 #sequence_revision 25-Apr-1997 #text_change
C;Accession: A45462
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C;Comment: This enzyme is a sesquiterpene cyclase involved in synthesis of the sesquite
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J. Biol. Chem. 268, 4543-4548, 1993
A;Title: Aristolochene synthase. Isolation, characterization, A;Reference number: A45462; MUID:93179472; PMID:8440737
A;Accession: A45462
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A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ECs2757 [imported] - Escherichia coli (strain 0157:H7, C;Species: Escherichia coli (C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P74312; EMBL:D90914; A;Note: the nucleotide sequence was submitted to
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A; Residues: 1-206 < KAN>
                                                                                                                                              A; Experimental source: strain
                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-103 <HAY>
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A; Residues: 1-342 < PRO>
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Best Local S
Matches 6
                                                                                                                                          ;Cross-references: UNIPROT:Q8X4V0; GB:BA000007; PIDN:BAB36180.1; PID:g13362225;
;Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                          EC82757
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Kasunaga, T.; Kuhara, S.;
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29; MUID:21156231; PMID:11258796
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23.3%; Pred. No. 47;
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hypothetical protein ECs2201 [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli (c;Species: Bscherichia coli (strain O157:H7, C;Species: Bscherichia co
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Query Match

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                                                                                                                                                                                                                                                                                                                           C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
C;Accession: C85713
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A; Residues: 1-103 <STO>
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001
C;Accession: A85821
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5; Conserv
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                           EKXXXXXXXXXXXXXXXBHPQFEK 28
                                                            Conservative
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Pred. No.
                                                                         Score 56;
Pred. No.
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7; Mismatches
                                                              Mismatches
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                                                                                                                                                       NID:g12515046; PIDN:AAG56167.1; GSPDB:(: EDL933
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                                                                                                                                                                                                                                                                                                 J.D.; Rose, Potamousis,
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Potamousis,
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C/Species: Brucella melitensis
                                                                                                                                                                                                                                        Delvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; I.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Call roc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
L'Title: The genome sequence of the facultative intracellular pathogen reference number: AD3252; PMID:11756688
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antho-RFamide neuropeptide 19 repeat precursor - sea anemone (Calliactis pa C;Species: Calliactis parasitica C;Date: 07-Feb-1992 #sequence_revision 07-Feb-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gasawara, N.; Yasunaga, T.; Kuhara, S.; Sniba, T.; Hattori, M.; Sninagawa, n. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90904
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A;Molecule type: DNA
A;Residues: 1-103 <HAY>
                                                                                                                                                   ;Cross-references: UNIPROT:Q8YEF6; GB:AE008917; PIDN:AAL53103.1; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: ECe2201
                                                                                  Keywords: acid-thiol
                                                                                                                                           Genetics:
                                                                                                                                                                                            Molecule type: DNA
Residues: 1-335 <KUR>
                                                                                                                                                                                                                                    Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            Species: Brucella;Date: 01-Feb-2002;Accession: AD3492
                                               Query Match
                                                                                                                      Gene: BMEI1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Darmer, D.; Schmutzler, C.; Diekhoff, D.; Grimmelikhuijzen, C.J.P.
roc. Natl. Acad. Sci. U.S.A. 88, 2555-2559, 1991
.Title: Primary structure of the precursor for the sea anemone neuropeptide Antho-RFami,Reference number: A39172; MUID:91172845; PMID:1706527
                                                                                                      Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Residues: 1-334 <DAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: UNIPROT:Q01133; GB:M59166; NID:g156133; PIDN:AAA27878.1; PID:g15613-
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         Similarity 7; Conserv
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         Conservative
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                                                                                                                                                                                                                                                                                                                                                                    #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
                                                                            ligase; coenzyme
   49.1%; Score 56; DB
26.9%; Pred. No. 53;
Live 13; Mismatches
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lzer, P.H.; Hagius, S.; O'Callaghan, D
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                                       DB 2;
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RIMD 0509952
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Gaps
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2005, 12:29:02

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A;Map position: 11L
A;Map position: 11L
F;1-35/Domain: WW repeat homology #status atypical
F:39-76/Domain: WW repeat homology <WW2>
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-583 <WIE>
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z28012; NID:g485996; PIDN:CAA81847.1; PID:g485997; MIPS:YKL012wA;Experimental source: strain S288C
R;Wiemann, S.; Voss, H.; Schwager, C.; Rupp, T.; Grothues, D.; Sensen, C.; Stegemann, J. submitted to the Protein Sequence Database, March 1994
A;Reference number: S37825
A;Accession: S37825
                                                                                                                                                                                                                                                                                          A;Gene: SGD:PRP40
                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z28012; NID:g485996; PIDN:CAA81847.1; PID:g485997; MIPS:YKL012w
A;Experimental source: strain S288C
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A; Residues: 1-583 <BOY>
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R;Boyer, J.; Pascolo, S.; Richard, G.F.; Ghazvini, M.;
submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-583 <PAS>
A;Residues: 1-583 <PAS>
A;Cross-references: UNIPROT:P33203; GB:S53418; NID:g263497; PIDN:AAB24902.1; PID:g263498
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Pascolo, S.; Ghazvini, M.; Boyer,
Yeast 8, 987-995, 1992
A;Title: The sequence of a 9.3 kb s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 09-Jul-2004
C;Accession: S30014; S37823; S37825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YKL012w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YKL165
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                                                                                                                                                Query Match
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                                                                                          49.1%; Score 56; 32.0%; Pred. No. ative 13; Mismatc
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Post-processing: :Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: uniprot_sprot:*
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Q6C664
Q6C7414
Q6FSP8
Q8RVC2
Q6FSP8
Q8RVE4
Q6FSP8
Q8RVE4
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Q8CJD2
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                                                                                                                                                                                                     OBtOW6 echinococcu
OBCJ02 rattus norv
OBCh90 rattus norv
O74je6 lactobacili
O62mt8 burkholderi
O62315 oryza sativ
O82315 oryza sativ
O82315 oryza sativ
O87m4 vibrio para
O1594 anthopleura
O1594 anthopleura
O73tf5 mycobacteri
O8wk9 marathrum s
O9bbg0 vanroyenell
O9bbg3 oserya coul
O83dg9 coxiella bu
O67d664 yarrowia li
p90984 caenorhabdi
O74345 schizosacch
Q8rvc2
Q6fsp8
Q8fsp8
Q8gch6
Q8gch6
Q89110
094524
Q6vt41
Q6vt41
Q6vt41
Q6vt41
Q6ft5
Q7n8a2
Q7n8a2
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1 vibrio para
1 candida gla
2 photorhabdu
5 caenorhabdi
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p maratrum ms
o vanroyanell
serya coul
coxiella bu
coxiella bu
coxiella bu
coxiella li
yarrowia li
schizosacch
coryza sativ
candida gla
staphylococ
bradyrhizob
neurospora
arabidopsis
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Regult No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32
56.5	56.5	56.5	57	57	57	57	57	57	57	57	57	57	57
49.6	49.6	49.6	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0
322	224	144	1698	719	652	590	541	355	305	305	247	206	192
N	N	N	<b>-</b>	μ	N	N	N	N	N	N	N	2	N
Q6CSW9	Q8RVV8	Q82GA4	CUL7 HUMAN	GLB2_XANAC	Q988Y6	Q6CVV1	Q987P4	Q9VXI0	Q6Z0Y9	Q8W403	Q82S44	P74312	Q6UUF7
Q6csw9	Q8rvv8	Q82ga4	Q14999	Q8pqa2	Q988y6	Q6cvv1	Q987p4		Q6z0y9	_	Q82s44	P74312	Q6uuf7
kluyveromyc	coffea arab	streptomyce	homo sapien	xanthomonas	rhizobium l	kluyveromyc	rhizobium l	drosophila	oryza sativ	oryza sativ	nitrosomona	synechocyst	oryza sativ

# ALIGNMENTS

SPIT		קם קם קם קם	ב ב ב ב ב ב ב ב ב ב ב ב ב ב ב ב ב ב ב	DR DR	# # # # # #	ב ק ק	, D D D	DR DR	DR P. P.	RT RA	2 × 0 0 0 0		RESULT Q8TOW6
011.	SM00261; FU; SM00219; TyrK S; PS00024; HE S; PS50011; PR	PF01030; Recep; ; PR00109; TYRK SM00060; FN3;	InterPro; IPR000719; Prot kinase. InterPro; IPR001245; Tyr pkinase. InterPro; IPR001266; Tyr pkinase_AS. Pfam: PF00757; Furin-like: 1.	IPR006212; IPR009030; IPR000585; IPR011009;	IPR003961; IPR008957; IPR006211;	Ď.	GO:0005006; GO:0004872; GO:0016740;	GO:0016020; GO:0005524;	locularis."; J. Parasitol. 33:301-312(2003). AJ458426; CAD30260.1;	SEQUENCE FROM N.A.  MEDILINE=22557731; PubMed=12670515; DOI=10.1016/S0020-7519(02)00265-5;  Konrad C., Kroner A., Spiliotis M., Zavala-Gongora R., Brehm K.;  "Identification and molecular characterisation of a gene encoding a member of the insulin receptor family in Echinococcus	Echinococcus multilocularis. Echinococcus multilocularis. Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda; Cyclophyllidea; Taeniidae; Echinococcus. NCBI TaxID=6211;	QBIOM6; 01-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Putative insulin receptor precursor.	OULT 1  OW6  OBTOW6  PRELIMINARY; PRT; 1749 AA.

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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nakamira I., Sizuki N.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ dat
EMBL; AB096020; BAC24016.1; -.
HSSP; B30803; 1AZS.
GO; GO:0004383; F:guanylate cyclase activity; IEJ.
GO; GO:0016829; F:lyase activity; IEA.
GO; GO:0007242; P:lyase activity; IEA.
GO; GO:0007242; P:lyase activity; IEA.
GO; GO:0007242; Guanylate cyclase.
InterPro; IPR001054; Gcyclase.
PEAM; PF00211; Guanylate cyc; 1.
R SMAXT; SM00044; CYCC; 1.
R PROSITE; PS00452; GUANYLATE CYCLASES 1; 1.
R PROSITE; PS00452; GUANYLATE CYCLASES 2; 1.
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Best Local S
Matches 8
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Soluble guanylyl cyclase alpha 2 subunit E219G mutant.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2003
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Guanylyl cyclase alpha 1 subunit.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Manmalla; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
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Q8CJD2;
01-MAR-2003
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  PF00211; Guanylate
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Rodentia;
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39.1%;
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Pred. No.
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Sciurognathi; Muridae; Murinae; Rattus
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X PubMed=14966310;
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A Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C. A Pridmore R.D., Berger B., Desiere F., Vilanova D., Barretto C. A Pridmore R.D., Berger B., C., Rouvet M., Altermann B., Barrango R., Wallet B., Mercenier A., Klaenhammer T., Arigoni F., Schell M. Tree genome sequence of the probiotic intestinal bacterium Lactobacillus johnsonii NCC 533.";
Froc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
R EMBL; AE017203; AAS08983.1;
R EMBL; AE017203; AAS08983.1;
R GO; GO:0001760; F:aminocarboxymuconate-semialdehyde decarboxy.
R GO; GO:0001760; F:aminocarboxymuconate-semialdehyde decarboxy.
R GO; GO:0001760; F:aminocarboxymuconate-semialdehyde decarboxy.
R GO; GO:00018152; P:metabolium; IEA.
R Interpro; IPRO02160; Prot inh Kunz-1g.
R PROSITE; PS00283; SOYBEAN KUNITZ; UNKNOWN 1.
Complete proteome; Hypothetical protein.
Complete proteome; Hypothetical protein.
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Matches 8
       SEQUENCE FROM N.A. STRAIN=ATCC 23344; Nierman W.C., DeSha Feldblyum T., Ulric
                                                                                                                                                                              Q62MT8;
25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DNA topoisomerase III (EC 5.99.1.2)
Name=topB; ORFNames=BMA0139;
Burkholderia mallei ATCC 23344.
                                                                                                                            NCBI_TaxID=243160;
                                                                                                                                                Bacteria; Proteobacteria; Betaproteobacteria;
Burkholderiaceae; Burkholderia.
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OrderedLocusNames=LJ1161;
Lactobacillus johnsonii.
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Q74JE6;
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PROSITE; PS00452; GUANYLATE CYCLASES 1;
PROSITE; PS50125; GUANYLATE_CYCLASES_2;
Lyase.

SEQUENCE 743 AA; 83251 MW; ACF5C53EC
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Ulrich R.
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Ronning C.
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Pred. No. 46;
14; Mismatches
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Pred. No. 70;
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Tettelin H., Nelson K.E.,
M., Brinkac L.M., Daugherty S.C.,
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A Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
A Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
A Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
A Chillingworth T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
A Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Rabbinowitech E., Rutherford K., Sanders M., Simmonds M.,
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
T "Genomic plasticity of the causative agent of melicidosis,
Burkholderia pseudomallei",
Durkholderia pseudomallei.",
L Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
R EMBL; BX571965; CAH34104.1; -.
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Q5-JUL-2004
Q5-JUL-2004
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DCL protein-like.
Name=0J1004_A11.16-2; Synonyms=P0539D10.35-2;
Oryza sativa (japonica cultivar-group).
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Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
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25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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"Structural flexibility in the Burkholderia mallei genome.";
Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
EMBL; CP000010; AAU48686.1; -.
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                                             (TrEMBLrel.
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Pred. No. 1.6e
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Lancet 361:743-749(2003).

EMBL; AP005079; BAC60017.1; ...

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004871; F:signal transducer activity; IE;

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR00163; EAL,

InterPro; IPR00163; EAL,

InterPro; IPR00360; His kin_HAMP.

Pfam; PP00563; EAL; 1.

Pfam; PP00903; GGDEF; 1.

R Pfam; PP009057; HAMP; 1.

SWART; SM00067; DUP2; 1.

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01-JUN-2003 (TrEMBLrel. 24, La
01-MAR-2004 (TrEMBLrel. 26, La
01-MAR-2004 (TrEMBLrel. 26, La
Hypothetical protein VP1754.
OrderedLocusNames=VP1754;
Vibrio parahaemolyticus.
Bacteria, Proteobacteria; Gamm
Vibrionaceae; Vibrio.
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SETRAIN-RIMD 2210633 / Serotype O3:K6;

MEDLINE-22508454; PubMed-12620739; DOI=10.1016/S0140-6736(03)12659-1;

MARKINO K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
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Submitted (MAR-2002) to the
EMBL; AP005287; BAD17315.1;
EMBL; AP004817; BAD17127.1;
SEQUENCE 107 AA; 12839 MW
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Sasaki T., Matsumoto
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the EMBL/GenBank/DDBJ
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Pfam; PF01581; FARP;
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MEDLINE=93054550; PubMed=1429603;

MEDLINE=93054550; PubMed=1429603;

Schmutzler C., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P.;

Schmutzler C., Darmer D., Diekhoff D., Grimmelikhuijzen C.J.P.;

"Identification of a novel type of processing sites in the precursor for the sea anemone neuropeptide Antho-RFamide (<Glu-Gly-Arg-Phe-NH2) from Anthopleura elegantissima.";

J. Biol. Chem. 267:22534-22541(1992).
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Q16934;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Antho-RFamide neuropeptides type 2 precursor.
Anthopleura elegantissima (Sea anemone)
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
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MEDLINE=87092339; PubMed=2879288;
Grimmelikhuijzen C.J.P., Graff D.;
"Isolation of pyroGlu-Gly-Arg-Phe-NH2 (Antho-RFamide),
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SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.
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eurosids [], Malpighiales; Podostemaceae; Marathrum.
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                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Kita Y., Kato M.;

"Phylogenetic relationships of the aquatic angiosperm family Podostemaceae inferred from matk sequence data.";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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SIMILARITY: Belongs to the intron maturase family 2. Matk
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                    as its content is in no way . Usage by and for commercial http://www.isb-sib.ch/announce/
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InterPro; IPR008998; Agglutinin.
InterPro; IPR00442; Intron_maturse2.
InterPro; IPR002866; MatK N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK N; 1.
Chloroplast; mRNA processing.
SEQUENCE 508 AA; 61342 MW; ECCF5B41
                                                                                                                                                                                                                                          09BBG3;
09BBG3;
01-JUN-2001
01-JUN-2001
01-MAR-2004
Chloroplast.
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosid
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01-JUN-2001
01-MAR-2004
                                                                                                                                         Oserya coulteriana.
                                                                                                                                                                            Name=matK;
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KATA Y., KATO M.;

KITA Y., KATO M.;

"Infrafamiliah Phylogeny of the Aquatic Angiosperm Podostemaceae
"Inferred from the Nucleotide Sequences of the matk Gene.";

Plant Biol. 3:156-163 (2001).

EMBL; ABO48379; BABB3398-1; -.

GO; GO:00095D7; C:chloroplast; IEA.

GO; GO:00083B0; P:RNA Eplicing; IEA.

GO:00083B0; P:RNA Eplicing; IEA.
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Pfam; PF01824; MatK_N; 1.
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InterPro; IPR000442; Intron_maturse2
InterPro; IPR002866; MatK_N.
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Eukaryota, Viridiplantae,
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8; Conserv
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Pred. No. 1.2e+02;
2; Mismatches 8
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"Infrafamilial Phylogeny of the Aquation Inferred from the Nucleotide Sequences Plant Biol. 3:156-163(2001).
EMBL; AB048375; BAB33395.1; -..
GO; GO:0009507; C:chloroplast; IEA.
GO; GO:00095080; P:RNA splicing; IEA.
                                                                                                                                                 Complete
SEQUENCE
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Q83DG9;
01-JUN-2003
01-JUN-2003
01-MAR-2004
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                                                                                                                                                                                                                                         PRINTS; PR00154; AMPBINDING.
TIGRFAMS; TIGR01217; ac_ac_CoA_syn;
                                                                                                                                                                                                                                                                                                                  GG; GO:0003824; F:catalytic activity; IEA.
GG; GO:0016405; F:CAA-ligase activity; IEA.
GG; GO:0008299; P:isoprenoid biosynthesis; IEA.
GG; GO:0008152; P:metabolism; IEA.
GD; GO:0008152; P:metabolism; IEA.
InterPro; IPR005914; Acac CoA synth.
InterPro; IPR005914; Acac CoA synth.
FFG0501; AMP-binding; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.E., Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Brinkac L.M., Maduu R., Dodson R.J., Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A., Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.; "Complete genome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Nine Mile phase I / RSA 493;
MEDLINE=22608657; PubMed=12704232;
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Coxiellaceae; Coxiella.
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
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ITY: Belongs to the
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llarity 28.6%;
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21.4%; Pr
1tive 17;
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Score 60; DB:
Pred. No. 1.6e
17; Mismatches
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Pred. No. 1.2e+02;
2; Mismatches 8;
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e ATP-dependent AMP-binding
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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## SUMMARIES

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## ALIGNMENTS

RESULT 1 ABP60369 02-OCT-2002. DE10113776-A1 Synthetic. Streptavidin; protein chip; microtitre plate; detection. Streptavidin binding peptide 28-MAR-2003 ABP60369; ABP60369 standard; peptide; 35 21-MAR-2001; 2001DE-01013776. 21-MAR-2001; 2001DE-01013776. Misc-difference (first entry) Location/Qualifiers /label= unknown /note= "optionally deleted for 1-15 residues" SEQ ID NO B 10

Schmidt

(BIOA-) INST BIOANALYTIK GMBH GOETTINGEN

WPI; 2003-031166/03.

protein, modules. New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding

Claim 7; Page 16; 18pp; German.

XAXEXEXXXXXXXEFFXEXEXEXEXEXEXEXEXEXEXEX The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion proteins (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides atronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it

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The invention relates to an isolated peptide (I) comprising at least two conditions in the containing at conditions and individual modules separated by 0-50 amino acids, with each containing at conditions one mostif His-Pro-X where X = Gln, Asn or Met. (I), which contain the conditions of the contain the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of attached proteins (II) (so it conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the condition in the conditions of the conditions of the conditions of the condition in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
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                                                                                                                                                                                                                                                                                       New isolated peptide, useful as affinity purification tag for recombinant protein, comprises at least two high-affinity streptavidin-binding
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                                                                                                                                                                                           A,
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein chip; microtitre plate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 9. .16 /label= unknown
                                                                                                   86.0%;
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44.4%; Pred. No. 1.5e-05;
tive 12; Mismatches 0;
                                                                         Score 98; DB
Pred. No. 1.5e
0; Mismatches
                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             affinity purification tag for recombinant high-affinity streptavidin-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                DB 6;
1.5e-05;
                                                                                                                       Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    detection.
                                                                         Indels
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                                                                      4,
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                                                                   Gaps
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WSHPOFEK----XXXXXXXXXXXXHPOFEK

24

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RESULT 5
ADB85492
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ABP60363
                                                                                                                                                                                               SXS
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                                                                                                            ક
                                                                                                                                          Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                 The invention relates to an isolated peptide (I) comprising at least two individual modules separated by 0-50 amino acids, with each containing at least one motif His-Pro-X where X = Gln, Asn or Met. (I), which contain streptavidin binding modules, are useful as affinity handles for purification of recombinant fusion protein (FP), also for detecting FP, e.g. on protein chips or microtitre plates. The modules in (I) bind strongly to streptavidin, with a co-operative effect that provides stronger binding than a single tag, but are displaced by a competitor. (I) does not interfere with the function of attached proteins (II) (so it may not be essential to remove it); facilitates detection and has easily controllable binding properties. (I) is particularly used for purifying FP from dilute solution in batch formats (which use simpler apparatus than column methods and result in lower loss of FP). The present sequence is that of a streptavidin binding peptide disclosed with the invention
ADB85492;
                       ADB85492 standard; protein; 763
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 4; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-031166/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001DE-01013776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAR-2001; 2001DE-01013776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptavidin binding peptide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABP60363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP60363 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE10113776-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOA-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INST BIOANALYTIK GMBH GOETTINGEN
                                                                                                                                                         Similarity
                                                                                                        WSHPQFEKXXXXXXXXXXXXXXXXBHPQ 25
                                                                                                                                                                                               24
                                                                                                                                            Conservative
                                                                                                                                                                                               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein chip; microtitre plate; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= unknown
                                                                                                                                                       60.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful as
least two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 AA
                                                                                                                                          0;
                                                                                                                                                       Score 69;
Pred. No.
                                                                                                                                            Mismatches
                       ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                              affinity purification tag for recombinant high-affinity streptavidin-binding
                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                   DB 6;
                                                                                                                                          0
                                                                                                                                                                  Length 24
                                                                                                                                          4.
                                                                                                                                          Gaps
                                                                                                                                          1:
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cartilage compressibility; cartilage elasticity; arthritic disease; osteoarthritis; cartilage degradation; inflammatory joint disease; aggrecanase-1; ADAMTS-4; aggrecanase-2; ADAMTS-5; thrombospondin domain; TSP domain; osteopathic; antiarthritic; cytostatic; antiinflammatory; antirheumatic; ophthalmological; thrombolytic; vasotropic; antimicrobial; respiratory-gen; nootropic; neuroprotective; antiparkinsonian; immunosuppressive; aggrecanase inhibition; cancer; rheumatoid arthritis; septic arthritis; corneal ulceration; coronary thrombosis; crohn's disease; emphysema; Alzheimer's disease; Parkinson's disease; multiple sclerosis; aortic aneurysm; enzyme; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human aggrecanase-2 (ADAMTS-5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           articular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                           proteoglycan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence
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04-DEC-2003 (first entry)

Synthetic. Homo sapiens.

Location/Qualifiers 756. .763 /label= Streptavidin Streptavidin\_tag

WO2003066822-A2

05-FEB-2003; 2003WO-US003554

05-FEB-2002; 2002US-0354592P

Georgiadis K, Crawford TK, Tomkinson Š Morris EA, Racie

WPI; 2003-731495/69.

New biologically-active aggrecanase protein having a deletion of all, a portion of a TSP domain, useful for treating osteoarthritis, cancer. Parkinson's disease, coronary thrombosis, Alzheimer's disease and multiple sclerosis. cancer, or

Disclosure; Fig 15; 111pp; English.

This invention relates to novel truncated human aggrecanase proteins and component of mucleotide sequences. Aggrecan is a major extracellular component of carticular cartilage. It is a proteoglycan responsible for providing contribution of the cartilage with its mechanical properties of compressibility and celasticity. The loss of aggrecan has been implicated in the degredation of articular cartilage in arthritic diseases such as osteoarthritis.

CC Aggrecanase is responsible for the cleavage of aggrecan, thereby having a color in cartilage degradation associated with osteoarthritis and confident of the current invention are truncated aggrecanase-1 (ADAMTS-4) and aggrecanase-2 (ADAMTS-5) enzymes which have at least one thrombospondin (TSP) domain deleted. These are composited their full-length counterparts. The proteins of the invention may be of cuse in the development of compounds with osteopathic, antiarthritic, cortostatic, antiinfammatory, antirheuratic, ophthalmological, antirocomic antiarthritic, antiinfammatory, antirheuratic, ophthalmological. thrombolytic, vasotropic, antimicrobial, respiratory-gen, nootropic, neuroprotective, antiparkinsonian or immunosuppressive activities through neuroprotective, antiparkinsonian or immunosuppressive activities through aggrecanase inhibition. The proteins of the invention may therefore be useful for the manufacture of compositions for the treatment of aggrecanase-associated conditions, such as osteoarthritis, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, corneal ulceration, coronary thrombosis, Crohi's disease, emphysema, the corneal ulceration, coronary thrombosis, Crohi's disease, emphysema, the corneal ulceration, coronary thrombosis, Crohi's disease, emphysema, the corneal ulceration, coronary thrombosis, Crohi's disease, emphysema, the corneal ulceration of the corneal ulceration of the corneal ulceration. Alzheimer's disease, Parkinson's disease, multiple sclerosis and aortic aneurysm. The present sequence is the amino acid sequence of a recombinant truncated aggrecanase 2 (ADAMTS-5) enzyme of the invention with a peptide linker and a streptavidin tag. and

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RESULT 6
ADS20249
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The invention relates to a novel isolated, modified ADAMTS4 (a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAMTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAMTS4 protein by at least one amino acid. ADAMTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The
                                                                                            Claim 9;
                                                                                                                      New isolated, modified ADAMTS4 (aggrecanase) stability useful for identifying inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type I motif 4; reprolysin; zinc metalloprotease; aggrecanase; osteopathic; antiinflammatory antiarthritic; antircytostatic; osteopathic; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's dig
                                                                                                                                                                                                                                                                                                                       29-JUL-2002; 2002US-0398721P
                                                                                                                                                                                                                                                                                                                                           29-JUL-2003; 2003WO-US023484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strep
                                                                                                                                                                                                                LAVA/)
                                                                                                                                                                                                                                                           (RACI/)
                                                                                                                                                                                                                                                                       (ZENG/)
                                                                                                                                                                                                                                                                                                                                                                                        WO2004011637'-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Furin-processed human aggrecanase ADAMTS4 truncated protein w Strep tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS20249;
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                                                                                                                                                          2004-143860/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743
                                                                                                                                                                                                             ZENG W.

RACIE L A.

MCDONAGH T.

FREEMAN B A.

GEORGIADIS K E
LAVALLIE E R.
                                                                                                                                                                                ΒA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome
                                                                                                                                                                                                                                                                             CORCORAN C
                                                                                      SEQ ID NO 47; 117pp; English
                                                                                                                                                                                                                                                                                                     HIETH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                               aggrecanase-associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGYTDVVRIPGSAWSHPQFEK 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KXXXXXXXXXXXXXBHPQFEK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           763
                                                                                                                                                                           Flannery CR,
Georgiadis KE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
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                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
475...485
/note= "Residues corresponding to positions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1q21-q23; enzyme; truncation; mature; furin cleavage;
                                                                                                                                                                                                                                                                              æ 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.6%;
                                                                                                                                                                            Zeng W, R
Lavallie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                485
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Pred. No. 37;
12; Mismatches
                                                                                                             conditions,
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                                                                                                                                                                            Racie LA,
e ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB
37;
                                                                                                          of the enzyme activity for including osteoarthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ٥,
                                                                                                                                                                                    Mcdonagh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                  687-837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease;
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Best Local S
Matches 11
                                            New isolated, modified ADAMTS4 (aggrecanase) stability useful for identifying inhibitors
                                                                                                             Corcoran
                                                                                                                                                                                                                                  29-JUL-2002; 2002US-0398721P
                                                                                                                                                                                            (CORC/)
                                                                                                                                                                                                                                                     29-JUL-2003; 2003WO-US023484.
                                                                                                                                                                                                                                                                                               WO2004011637-A2
                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                            aggrecanase; osteopathic; antiinflammatory; antiarthritic; anticytostatic; osteoarthritis; glioma; cancer; inflammatory joint; rheumatoid arthritis; septic arthritis; periodontal; Crohn's di
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Unidentified
                                                                                                                                                                                    (ZENG/)
                                                                                                                                                                                                                                                                                                                                                                                                                          ADAMTS4; a disintegrin-like and metalloprotease; thrombospondin type 1 motif 4; reprolysin; zinc metalloprotease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein of the invention demonstrates osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of the furin-processed human aggrecanase ADAMTS4 truncated protein with Strep tag of the invention.
                                                                                                                                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS20227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 485 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             456
                                                                                                                               FREEMAN B A.
GEORGIADIS K I
LAVALLIE E R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggrecanase ADAMTS4 truncated
                                                                                                                                                                                          CORCORAN C
                                                                                                                                                                                                                                                                                                                                                                                        enzyme;
                                                                                                   BA,
                                                                                                                                                              MCDONAGH T
                                                                                                        5
                                                                                                                                                                                   ZENG W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHPQFEK---XXXXXXXXXXXXXXXXBHPQFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein;
                                                                                               Flannery C
Georgiadis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 687. .697
                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                           72 C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.2%;
36.7%;
                                                                                                 E CR
                                                                                                                                                                                                                                                                                                            "Wild-type residues 687-837 replaced by Strep tag"
                                                                                                                                                                                                                                                                                                                                                                                     1q21-q23; truncation;
                                                                                               Zeng W, R
Lavallie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 67.5;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                               Racie LA,
e ER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein with Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                       Mcdonagh
                                                                                                                                                                                                                                                                                                                                                                                     Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                    tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         tag
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                                                                                                                                                                                                                                                                                                                                                                                                                antirheumatic;
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The invention

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a novel

isolated,

modified ADAMTS4 (a

Claim

9; SEQ

ID NO 24; relates

117pp; English

aggrecanase-associated

conditions,

) protein with improved of the enzyme activity for including osteoarthritis.

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RESULT 8
AAE24889
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif 4) protein with improved stability compared to a naturally occurring, full-length ADAWTS4 protein, where the modified protein differs from the naturally-occurring, full-length ADAWTS4 protein by at least one amino acid. ADAWTS proteins are a subfamily of zinc metalloproteases and include aggrecanases amongst their members. The protein of the invention demonstrates osteopathic, antiinflammatory, antiarthritic, antirheumatic and cytostatic activities and may be useful for treating aggrecanase-associated conditions, including osteoarthritis, glioma, cancer, inflammatory joint disease, rheumatoid arthritis, septic arthritis, periodontal disease and Crohn's disease. The current sequence is that of the human aggrecanase ADAWTS4 truncated protein with Strep tag of the invention.
                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                         Misc-difference
                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choline-binding protein; CbpG; vaccine; immune response; infection; antibacterial; CbpA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 697 AA;
                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-2003
22-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE24889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAE24889 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pneumococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sp. choline-binding protein, CbpA #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Unknown
/note= "Encoded by TGA of the inverse complementary
strand of the sequence shown in Fig 1 (AAD40149)"
27
                                                       /label= Unknown
/note= "Encoded by TGA
strand of the sequence
                                                                                                                                                                                                 /label= Unknown
/note= "Encoded by TGA of the inverse complementary
strand of the sequence shown in Fig 1 (AAD40149)"
108
                                                                                                                                                                                                                                                                                           /label= Unknown
/note= "Encoded by TGA of the inverse
strand of the sequence shown in Fig 1
                                                                                                                                                                                                                                                                                                                                                                        /label= Unknown
/note= "Encoded by TGA
strand of the sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                   /label= Unknown
/note= "Encoded
strand of the se
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Encoded by TGA strand of the sequence
/label= Unknown
/note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Unknown
/note= "Encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.2%;
36.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67.5;
Pred. No. 38;
                                                                                                                                   led by TGA
δ
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  TGA of the
                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the inverse shown in Fig 1
                                                                                                                                     of the inverse
shown in Fig 1
                                                                                                                                                                                                                                                                                                                                                                          of the inverse
shown-in Fig 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                       e inverse
in Fig 1
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inverse complementary
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                                                                                                                                   Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        complementary (AAD40149)"
                                                                                                                                     complementary (AAD40149)"
                                                                                                                                                                                                                                                                                              (AAD40149) "
                                                                                                                                                                                                                                                                                                                                                                            (AAD40149)"
                                                         (AAD40149)"
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RESULT 9
AAG80260
ID AAG8
XX
AC AAG8
XX
DT 18-F
XX
Chim
XX
Corr
KW Pota
KW Pota
KW infl
XX
Homc
OS Homc
OS Stre
OS Synt
XX
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                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to choline-binding protein (CbpG) and its corresponding nucleic acid. Vaccines that contain CbpG, its N- truncated version or nucleic acid encoding them are useful for preventing infection by bacteria that express CbpG, specifically Streptococcus pneumoniae and in inducing an immune response. Compositions that contain CbpG or antibodies specific for it are useful for treating such infections. Antibodies are also useful for diagnostic detection of CbpG and oligonucleotides that hybridise to CbpG DNA are used to detect CbpG-expressing bacteria. CbpG DNA are used for recombinant production of CbpG and their fragments. The present sequence is Pneumococcus sp. CbpA protein. (Updated on 06-AUG-2003 to correct OS field.)
             Homo sapiens.
Streptomyces lividans
Synthetic.
                                                                                Potassium channel; chimeric; KcsA; Kv3.1; agonist; antagonist; tumour; circulatory disorder; nervous system disorder; urinary incontinence;
                                                                                                                        Chimeric potassium
                                                                                                                                                    18-FEB-2002
                                                                                                                                                                                AAG80260;
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated streptococcal choline-binding protein CbpG, treatment of streptococcal infections and in protective related nucleic acid and antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                          AAG80260 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Fig 1; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD40149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tuomanen EI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TUOM/) TUOMANEN E I.
(GOSI/) GOSINK K.
(MASU/) MASURE R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2002041881-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-488715/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 8661-AON-61
                                                                                                                                                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                    Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                            179
                                                                                                                                                                                                                                                                                                         WSHPQFEKXXXXXXXXXXXXXXXHP
                                                                                                                                                                                                                                                                                WSHPVAIEPLAFRXYHEPLYWSHP
                                                                                                                                                                                                                                                                                                                                    57.9%; ilarity 37.5%; Conservative 1:
                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                    (first entry)
                                                                isorder; nervous system disorder; protein chip; screening; ChiVI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gosink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-00196389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9905-00287070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Unknown
/note= "Encoded by TGA
strand of the sequence
179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Encoded by GT of the inverse complementary strand
of the sequence shown in Fig 1 (AAD40149)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strand of the sequence shown in Fig 1 (AAD40149)"
                                                                                                                          channel KcsA-Kv1/3 ChiVI.
                                                                                                                                                                                                          protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Masure
                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                  Score 66;
Pred. No.
                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                         24
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                                                                                                                                                                                                                                                                                                                                               DB
7.8;
                                                                                                                                                                                                                                                                                                                                                                5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e inverse
in Fig 1
                                                                                                                                                                                                                                                                                                                                                                Length 179;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AAD40149)".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccines,
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                                                                                                                                                                                                                                                                                                                                      Gaps
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RESULT 10
AAG80261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel chimeric nucleic acid (I), encoding a CC potassium channel subunit (II) derived from Streptomyces lividans KCsA CC and human KV1.3. The chimeric (bacterial-human) potassium channels are CC useful, after fixing to a carrier, for identifying compounds that bind to the chimeras or modify their activity, i.e. compounds that are toxic or compounds that are toxic or contentially useful therapeutically, by acting as potassium channel CC antagonist or agonist, in treatment of circulatory or nervous system CC disorders, urinary incontinence, tumours, or inflammation, in human or continery medicine. Chimeric channels encoded by (I) can be immobilized, cetive and functional form, and membranes by protein chip CC technology. The channels can be isolated from recombinant bacteria in CC weeks or months, during which time they can be used many times. This confidence represents ChiVI subunit used in the construction of the chimeric potassium channels described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
24-MAY-2000; 2000DE-01025620
                          24-MAY-2000; 2000DE-01025620.
                                                                                                                  Homo sapiens.
Streptomyces lividans.
Synthetic.
                                                         06-DEC-2001
                                                                                    DE10025620-A1
                                                                                                                                                             Potassium channel; chimeric; KcsA; Kv3.1; agonist; antagonist; tumou circulatory disorder; nervous system disorder; urinary incontinence; inflammation; protein chip; screening; ChiVII.
                                                                                                                                                                                                                           Chimeric potassium channel KcsA-Kv1/3 ChiVII.
                                                                                                                                                                                                                                                          18-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                   AAG80261 standard; protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 15; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding chimeric potassium channel protein, when immobilized on carrier, in screening agents for toxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ponga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2001.
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DB; AAI69255.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                 HERFORLERMLDDNRRSAWRHPOF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Legros C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.9%; Score 66; D
29.2%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eauclaire M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Mismatches
                                                                                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bougis PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                              2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 183
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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CC This invention describes a novel chimeric nucleic acid (I), encoding a CC potassium channel subunit (II) derived from Streptomyces lividans KCsA CC and human KV.13. The chimeric (bacterial-human) potassium channels are CC useful, after fixing to a carrier, for identifying compounds that bind to the chimeras or modify their activity, i.e. compounds that are toxic or CC potentially useful therapeutically, by acting as potassium channel CC antagonist or agonist, in treatment of circulatory or nervous system CC disorders, urinary incontinence, tumours, or inflammation, in human or CC veterinary medicine. Chimeric channels encoded by (I) can be immobilized, CC as an array, on a carrier, making possible screening by protein chip CC as an array, on a carrier, making possible screening by protein chip CC technology. The channels can be isolated from recombinant bacteria in CC weeks or months, during which then they can be used many times. This CC sequence represents the ChivII subunit used in the construction of the CC chimeric potassium channels described in the invention
Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding chimeric potassium channel protein, useful, when immobilized on carrier, in screening agents for toxicity and pharmaceutical activity.
                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 16; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH
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DB; AAI69256.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bougis PE
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밁 Ş Query Match Best Local S Matches 7 158 3 HPQFEKXXXXXXXXXXXXXXXHPQF 26 Similarity 7; Conserv | :|::::::::::| |||| HERFDRLERMLDDNRRSAWRHPQF 181 Conservative 57.9%; Score 66; 29.2%; Pred. No. 15; Mismatches DB 5; ν •• Length 183 Indels 0 Gaps

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RESULT 11
AAG80255
Chimeric potassium channel KcsA-Kv1/3 Chir.
                               18-FEB-2002
                                                                               AAG80255 standard;
                           (first entry)
                                                                             protein;
                                                                             A
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circulatory disorder; inflammation; protein Potassium channel; chimeric; KcsA; Kv3.1; agonist; antagonist; tumour; circulatory disorder; nervous system disorder; urinary incontinence; Homo sapiens nervous system disorder; urinary chip; screening; ChiI.

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Pongs O,
                             24-MAY-2000; 2000DE-01025620.
                                      24-MAY-2000; 2000DE-01025620
                                                 06-DEC-2001.
                      (GENI-)
                                                          DE10025620-A1
                                                                   Streptomyces lividans. Synthetic.
                   FORSCHUNGSGESELLSCHAFT GENION MBH
           Legros C,
            Eauclaire
           Z,
           Bougis PE,
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WPI; 2002-042513/06. N-PSDB; AAI69250.

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RESULT 12
AAG80258
8
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel chimeric nucleic acid (I), encoding a potassium channel subunit (II) derived from Streptomyces lividans KcsA and human Kvl.3. The chimeric (bacterial-human) potassium channels are useful, after fixing to a carrier, for identifying compounds that bind to the chimeras or modify their activity, i.e. compounds that are toxic or potentially useful therapeutically, by acting as potassium channel antagonist or agonist, in treatment of circulatory or nervous system disorders, urinary incontinence, tumours, or inflammation, in human or veterinary medicine. Chimeric channels encoded by (I) can be immobilized, as an array, on a carrier, making possible screening by protein chip technology. The channels can be isolated from recombinant bacteria in stable, active and functional form, and membranes are stable for many weeks or months, during which time they can be used many times. This sequence represents the ChiI subunit used in the construction of the
                                             New nucleic acid encoding ch:
when immobilized on carrier,
pharmaceutical activity.
                                                                                                                                                                                                                                                        24-MAY-2000; 2000DE-01025620
                                                                                                                                                                                                                                                                                                                       DE10025620-A1
                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                      Streptomyces lividans.
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  Potassium channel; chimeric; KcsA; Kv3.1; agonist; antagonist; tumour; circulatory disorder; nervous system disorder; urinary incontinence; inflammation; protein chip; screening; ChiIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric potassium channel KcsA-Kv1/3 ChiIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG80258 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 12; 34pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding chimeric potassium channel protein, useful, when immobilized on carrier, in screening agents for toxicity and
                                                                                                           WPI; 2002-042513/06.
N-PSDB; AAI69253.
                                                                                                                                                                                                                         24-MAY-2000; 2000DE-01025620
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             Example 1; Page 14; 34pp; German
                                                                                                                                                                                          (GENI-) FORSCHUNGSGESELLSCHAFT GENION MBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            potassium channels described in the invention
                                                                                                                                                           Legros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                          ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                           Eauclaire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.9%; Score 66; 29.2%; Pred. No.
                                                         chimeric potassium channel protein, useful, 
er, in screening agents for toxicity and
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                                                                                    New nucleic acid encoding chimeric potassi when immobilized on carrier, in screening pharmaceutical activity.
                                                                                                                                                                                                                                                                                                                                                                                        Key Location/Qualifiers Misc-difference 181
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V-PSDB; AAI69258.
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This invention describes a novel chimeric nucleic acid (I), encoding a potassium channel subunit (II) derived from Streptomyces lividans KcsA and human Kv1.3. The chimeric (bacterial-human) potassium channels are

Example

2; Page 17; 34pp; German.

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RESULT 14
AAG80262
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This invention describes a novel chimeric nucleic acid (I), encoding a potassium channel subunit (II) derived from Streptomyces lividans KcsA and human Kv1.3. The chimeric (bacterial-human) potassium channels are useful, after fixing to a carrier, for identifying compounds that bind to the chimeras or modify their activity, i.e. compounds that are toxic or potentially useful therapeutically, by acting as potassium channel arragonist or agonist, in treatment of circulatory or nervous system disorders, urinary incontinence, tumours, or inflammation, in human or veterinary medicine. Chimeric channels encoded by (I) can be immobilized, as an array, on a carrier, making possible screening by protein chip
                                                                                                                                                                                                                                                                                          Example 1; Page 16; 34pp;
                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding ch
when immobilized on carrier,
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|HERFDRLERMLDDNRRSAWRHPQF 181
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                            This invention describes a novel chimeric nucleic acid (I), encoding a C potassium channel subunit (II) derived from Streptomyces lividans KCSA CC and human KV1.3. The chimeric (bacterial-human) potassium channels are CC useful, after fixing to a carrier, for identifying compounds that bind to the chimeras or modify their activity, i.e. compounds that are toxic or CC potentially useful therapeutically, by acting as potassium channel contagonist or agonist, in treatment of circulatory or nervous system CC disorders, urinary incontinence, tumours, or inflammation, in human or CC veterinary medicine. Chimeric channels encoded by (I) can be ismobilized, CC as an array, on a carrier, making possible screening by protein chip CC technology. The channels can be isolated from recombinant bacteria in CC stable, active and functional form, and membranes are stable for many CC weeks or months, during which time they can be used many times. This CC sequence represents the Chix subunit used in the construction of the CC chimeric potassium channels described in the invention
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Pred. No. 8;
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		arch completed: March 2, 2005, 13:0 b time : 126.114 secs	Query Match 57.9%; Score 66; DB 5; Length 183; Best Local Similarity 29.2%; Pred. No. 8; Matches 7; Conservative 15; Mismatches 2; Indels 0; Gaps 0; Matches 7; Conservative 25; Mismatches 2; Indels 0; Gaps 0; Qy 3 HPOFEXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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Perfect score:
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seq length: 2000000000
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| Ggn2_6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*
| Ggn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| Ggn2_6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
| Ggn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
| Ggn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
| Ggn2_6/ptodata/2/pubpaa/US07 NEW PUB.pep:*
| Ggn2_6/ptodata/2/pubpaa/US08 NEW PUB.pep:*
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4 US-10-026-578B-10
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17 US-10-887-228A-5
14 US-10-687-228A-5
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Sequence 10, Appli
Sequence 3, Appli
Sequence 11, Appl
Sequence 31, Appl
Sequence 31, Appli
Sequence 4, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 4, Appli
Sequence 15, Appli
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
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Sequence 201843,	ø	equence	æ	e 70843,	equence 62543,	e 71583,	equence 66584,	e 61196,	Sequence 42846, A	e 50330,	æ		10		Sequence 8, Appli					Sequence 9, Appli		equence	Ф	equence	æ	equence	equence	æ	e 1847	equence 27, App	Sequence 40, Appl

## ALIGNMENTS

RESULT 1 US-10-026-578B-10

Sequence 10, Application US/10026578B Publication No. US20030083474A1

GENERAL INFORMATION:

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APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
CURRENT REFERENCE: 100810.01US1
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR PILING DATE: 2001-0-12
NUMBER OF SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NOS: 14
SEQ ID NO 10
LENGTH: 36
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Synthetic Peptide
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (9). - (28)
COTHER INFORMATION: a represents a single amino acid at each of the positions indicat OTHER INFORMATION: missing, the total numbers of x will be no less than 5
PRATURE: NAME/KEY: misc feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
US-10-026-578B-10

Ouery Match
Best Local Similarity 77.8%; Pred. No. 6.6e-05;
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                                                                                                    US-10-026-578B-3
                   Query Match
Best Local Similarity 85.7
24; Conservative
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 24
TYPE: PRT
                                                                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Artificial Sequence represents
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                                                                                                                                                      OTHER INFORMATION: X represents a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/026,578B CURRENT FILING DATE: 2002-11-11
                                                                                                                                                                            NAME/KEY: MISC FEATURE
                                                                                                                                                                                                                     OTHER INFORMATION: X represents
                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE OCATION: (15)..(15)
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LOCATION: (14)...(14)
                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: X represents a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity TaFILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (11) ... (11)
OTHER INFORMATION: X represents a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: MISC_FEATURE
LOCATION: (10) - (10)
OTHER_INFORMATION: X represents a single amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER_INFORMATION: X represents a single amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                             OCATION: (12)..(12)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                        INFORMATION: X represents a single amino
1 WSHPQFEKXXXXXXXXXXXXXXXBHPQFEK 28
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-809-517A-31
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                                                                                                                                    APPLICAMY: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 1999-07-20
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
SUDTMARE: Patentin version 3.0
SEQ ID NOS: 41
SOFTMARE: Patentin version 3.0
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  Query Match
Best Local Similarity
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US-10-026-578B-11
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Sequence 31, Application US/09809517A
Patent No. US20020034733A1
GENERAL INFORMATION:
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Best Local
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SEQ ID NO 11
                                                                                                               LENGTH: 24
TYPE: PRT
ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity '
EILE REFERENCE: 100810, 01051
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PPLICATION NUMBER: PCT/EP01/11846
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
OTHER INFORMATION: Artificial Sequence represents peptide binding module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Of the five OTHER INFORMATION: repeats may OTHER INFORMATION: be present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IBA (GmbH)
APPLICANT: Schmidt,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: MISC FEATURE LOCATION: (9). (28)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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    67.5%;
41.7%;
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Score 77;
Pred. No.
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Pred. No.
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DB 9;
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FILE REFERENCE: $30569US
CURRENT APPLICATION NUMBER: US/10/887,228A
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: DE 103 31 093.2
PRIOR FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 60/478,262
PRIOR FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PALENTIN version 3.1
SEQ ID NO 1
LENGTH: 245
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LENGTH: 25
TYPE: PRT
ORGANISM: artificial sequence
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Best Local Similarity
Matches 10; Conserv
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Best Local &
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CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Schering AG
TITLE OF INVENTION: Device and Process for Direct Quantitative in vitro
TITLE OF INVENTION: Substance That is Contained in a Sample
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TITLE OF INVENTION: No. US20020034733Alel methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
                                                                                                                                                     OTHER INFORMATION: Fab fragment of variable heavy chain
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EFEQKLISEEDLNGAPWSHPQFEK 245
                            QFEKXXXXXXXXXXXXWSHPQFEK 28
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                                                                    Conservative
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                                                                                67.5%; Score 77;
41.7%; Pred. No.
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41.7%; Pred. No. 0.
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CURRENT APPLICATION NUMBER: US/10/887,228A
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: DE 103 31 093.2
PRIOR FILING DATE: 2003-07-09
PRIOR APPLICATION NUMBER: US 60/478,262
PRIOR FILING DATE: 2003-07-16
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
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; SEQ ID NO 9
TENCTH: 246
                                                                 Query Match
Best Local Similarity
Matches 10; Conserv
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 252
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APPLICANT: Schering AG
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Best Local Similarity 41.7%; Pred. No. 0.
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CURRENT APPLICATION NUMBER: US/10/887,228A
CURRENT FILING DATE: 2004-07-09
PRIOR APPLICATION NUMBER: DE 103 31 093.2
PRIOR FILING DATE: 2003-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schering AG
TITLE OF INVENTION: Device and Process for Direct Quantitative in vitro Determinatio
TITLE OF INVENTION: Substance That is Contained in a Sample
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                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/478,262 PRIOR FILING DATE: 2003-07-16
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                                                                                                                                                                                         TYPE: PRT
ORGANISM: artificial
FEATURE:
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EFEQKLISEEDLNGAPWSHPQFEK 252
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                                                                             Conservative
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                                                                                         67.5%;
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Pred. No. 0
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RESULT 9 US-10-026-578B-4

, Sequence 4, Application US/10026578B

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APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
SOFTWARE: Patentin version 3.1
                                                     NAME/KEY: MISC_FEATURE
                                                                                OTHER INFORMATION: X represents a
                                                                                                        FEATURE: NAME/KEY: MISC_FEATURE
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                   EATURE:
                                                                                                                                                        NAME/KEY: MISC FEATURE
LOCATION: (22)...(22)
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OTHER INFORMATION: X represents
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LOCATION: (16) ... (16)
OTHER INFORMATION: X represents a single
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OTHER INFORMATION: X represents
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LOCATION: (17)...(17)
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OTHER INFORMATION: Synthetic Peptide
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (9)...(9)
OTHER INFORMATION: X represents a single amino (
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OTHER INFORMATION: X represents
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LOCATION: (13)...(13)
OTHER_INFORMATION: X represents a single
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LOCATION: (10)...(10)
OTHER INFORMATION: X represents a single
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OTHER INFORMATION: X represents
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OTHER INFORMATION: X represents a
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TYPE: PRT
ORGANISM: Artificial Sequence
                    INFORMATION: X represents a single amino acid at the
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RESULT 12
US-10-628-432-24
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US-10-628-432-47
                                                                                                            Query Match
Best Local S
Matches 11
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-358-283-15
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                                                                                                                          Similarity
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APPLICANT: Wyeth

ITTLE OF INVENTION: Modified ADAMTS4 molecules

FILE REFERENCE: AM101378

CURRENT APPLICATION NUMBER: US/10/628,432

CURRENT FILING DATE: 2003-07-29

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.1

LENGTH: 485

TYPE: PRT

ORGANISM: Artificial

FEATURE:
OTHER INFORMATION: furin-processed construct C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-358-283-15; Sequence 15, Application US/10358283; Publication No. US20040054149A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc feature
; OTHER INFORMATION; Artificial Sequence represents peptide binding module
US-10-026-578B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/358,283
CURRENT FILING DATE: 2003-02-17
PRIOR APPLICATION NUMBER: 60/354,592
PRIOR FILING DATE: 2002-02-05
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WYETH
TITLE OF INVENTION: TRUNCATED AGGRECANASE MOLECULES
FILE REFERENCE: 08702-0112-00000
456 SKKKFDKCMVCGGDGSGCSGSAWSHPQFEK 485
                           8 KXXXXXXXXXXXXXXXXBHPQFEK 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WSHPQFEKXXXXXXXXXXXXXXSHPQ 25
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                                                                                                                                                                                                                                                                                                                                                     Application US/10628432
No. US20040142863A1
                                                               Conservative
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                                                                          59.2%;
36.7%;
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42.9%; Pred. No.
tive 12; Mismatc
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Pred. No. 30;
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Pred. No. 0.34
0; Mismatches
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RESULT 13

US-10-628-432-49',
Sequence 49, Application US/10628432

Publication No. US20040142863A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24, Application US/10628432
Publication No. US20040142863A1
GENERAL INFORMATION:
APPLICANT: Wyeth
ITITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
CURRENT FILING DATE: 2003-07-29
CURRENT FILING DATE: 303-07-29
CURRENT FILING DATE: 303-07-29
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US-10-628-432-40
; Sequence 40, Application US/10628432
; Publication No. US20040142863A1
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: furin-processed construct
US-10-628-432-49
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                                                               APPLICANT: Wyeth
TITLE OF INVENTION: Modified ADAMTS4 molecules
FILE REFERENCE: AM101378
CURRENT APPLICATION NUMBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.1
SEQ ID NO 40
LENGTH: 845
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Best Local Similarity
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TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      615 WLHRRAQILEILRRRPWAGRKGSAWSHPQPEK 646
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31.2%; Pred. No.
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: OTHER INFORMATION: ADAMTS4 ASM with insertion US-10-628-432-40 \,
Search completed: March Job time: 88.0732 secs
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                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Modified ADAMTS4 molecules FILE REFERENCE: AMIO1378
CURRENT APPLICATION INWEBER: US/10/628,432
CURRENT FILING DATE: 2003-07-29
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                           Sequence 27, Application US/10628432
Publication No. US20040142863A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Matches 9; Conserv
                                                                                                                     Matches
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Best Local Similarity
                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                       LENGTH: 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  520 WSHPQFEKAGGWGPWGPWGDCS 541
                                                        827 WIHRRAQILEILRRRPWAGRKGSAWSHPQFEK 858
                                                                                                                   10;
                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.0%; Score 65; DB llarity 40.9%; Pred. No. 1.30 Conservative 12; Mismatches
              'n
                                                                                                                                   57.0%; Score 65; DB 16; 31.2%; Pred. No. 1.3e+02;
              2005, 14:19:04
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1.3e+02;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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     GenCore version 5.1.6
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US-09-977-137A-1
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laying laying Indel	2 209-517A-34 it No. 6753136 tL INFORMATION: LICANT: Lohning, Corinna LICANT: Lohning, Corinna LICANT: Lohning, No. 6753136el methods LE OF INVENTION: particles via disulf REFERENCE: MORPHO/11 RENT APPLICATION NUMBER: US/09/809,517 RENT FILING DATE: 2001-03-15 DR APPLICATION NUMBER: EP 99114072.4 DR FILING DATE: 199-07-20 DR PILING DATE: 2000-02-18 DR FILING DATE: 2000-02-18	NO9-517A-31 109-517A-31 11 NO. 6753136 11 NO. 6753136 12 CANT: Lohning, Corinna 12 COF INVENTION: 12 COF INVENTION: 13 REFERENCE: MORPHO/11 18 RAPLICATION NUMBER: US/09/809,517A 18 FILING DATE: 2001-03-15 18 RAPPLICATION NUMBER: EP 9914072.4 18 RILING DATE: 1999-07-20 19 RAPPLICATION NUMBER: EP 00103551.8 18 FILING DATE: 1999-07-20 19 RAPPLICATION NUMBER: EP 00103551.8 18 FILING DATE: 1000-02-18 18 RAPPLICATION NUMBER: EP 00103551.8 19 FILING DATE: 2000-02-18 19 FRT 18 ANISM: artificial sequence 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NOS: 41 10 NO	54 47.4 259 4 US-09-431-887-33 Sequence 33 53.5 46.9 155 3 US-09-160-567-11 Sequence 11 53.5 46.9 155 4 US-09-710-299-11 Sequence 11 53.5 46.9 155 4 US-09-710-299-11 Sequence 11 53.5 46.9 495 3 US-09-160-567-4 Sequence 4 53.5 46.9 495 3 US-09-160-567-4 Sequence 4 53.5 46.9 495 4 US-09-100-299-4 Sequence 4 53.5 46.9 495 4 US-09-710-299-4 Sequence 4 53.4 46.9 495 4 US-09-710-299-4 Sequence 4 53.5 46.9 495 4 US-09-710-299-4 Sequence 4 53.4 46.5 203 4 US-09-509-31-6 Sequence 33 53.4 46.5 203 4 US-09-270-767-33748 Sequence 54 53.4 46.5 297 4 US-09-270-767-33748 Sequence 54 53.4 46.5 297 4 US-09-107-532A-4868 Sequence 54 53.4 46.5 483 4 US-09-107-532A-4868 Sequence 18 53.4 6.5 527 4 US-09-600-985-1 Sequence 18 53.4 6.5 527 4 US-09-600-985-3 Sequence 23 53.4 6.5 527 4 US-09-600-985-3 Sequence 3, 53.4 6.5 527 4 US-09-600-985-3 Sequence 3, 53.4 6.5 527 4 US-09-600-985-3 Sequence 3,

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CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 22
TYPE: PRT
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CURRENT APPLICATION NUMBER: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOPTWARE: PatentIn version 3.0
LENGTH: 21
TYPE: PRT
ORGANISM: artificial sequence
PRATURE: Artificial sequence
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                                                                                                                                                                                                                  Sequence 33, Application US/09809517A
Patent No. 6753136
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. 6753136el methods for displaying (poly)peptides/proteins on
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
FILE REFERENCE: MORPHO/11
FILE REFERENCE: MORPHO/11
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-809-517A-34
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Patent No. 67531
ORGANISM: artificial sequence
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41.7%; Pred. No. 0.0014;
7ative 14; Mismatches
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Pred. No.
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                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: US-09-977-137A-5
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTMARE: PATENTIN Ver. 2.0
SEQ ID NO 4
SEQ ID NO 4
LENGTH: 117
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PRIOR ETILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic module
US-09-809-517A-33
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09977137A Patent No. 6750042
                                                                                                                                                                                                                                          APPLICANT: Summers, Anne O.
APPLICANT: Cagulat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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APPLICANT: Summers, Anne
APPLICANT: Caguiat, Jona
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Best Local S
                                                                                                                        LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                FEATURE:
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: chelon
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o. 6750042
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8; Conserv
        55.3%; Score 63; DB 4; ilarity 40.0%; Pred. No. 1.5; Conservative 12; Mismatches
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Pred. No. 1.5;
12; Mismatches
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US-09-977-137A-8
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US-09-977-137A-7
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SEQ ID NO 7
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                         Query Match
Best Local (
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APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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Best Local
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                                                            Matches
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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APPLICANT: Caguiat, Jonath
                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No.
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RESULT 9

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RESULT 11
US-09-977-137A-11
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US-09-977-137A-10
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Sequence 11, Application US/09977137A
PATENT NO. 6750042
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 10
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APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonath
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Patent No. 6750042
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Matches 8; Conserv
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Metal Binding Proteins, TITLE OF INVENTION: Methods FILE REFERENCE: 79-00
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
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TYPE: PRT
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40.0%; Pred. No. 1.5
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Pred. No. 1.5;
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Best Local Similarity
Watches 8; Conserve
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US-09-977-137A-12
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US-09-977-137A-12
Sequence 6, Application US/09977137A
Patent No. 6750042
GEMERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells.
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION UNMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
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LENGTH: 117
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
LENGTH: E117
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
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ORGANISM: Artificial Sequence
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FILE REFERENCE: 79-0
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ORGANISM: Artificial Sequence
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40.0%; Pred. No. 1
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GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO C

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A.

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER: OF SEQ ID NOS: 28208

SEQ ID NO 22626

LENGTH: 1298

TWITTE TOTAL

LENGTH: 1298

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TO COMMENT OF SEQ ID NOS: 28208
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                                                                                                                               ; LENGTH: 168
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-31955
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US-09-248-796A-22626
                                                                                                                                                                                                ; Sequence 31955, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 31955
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US-09-248-796A-22626
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Best Local
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                                                             Matches
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Patent No. 6747137
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TYPE: PRT
ORGANISM: Artificial Sequence
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1 WSHPQFEKXXXXXXXXXXXXXXWSHPQF
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